seq1-f.rapb

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GenCore version 5.1.6
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                   Copyright
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OM protein - protein search, using sw model

October 13, 2004, 11:23:49; Search time 138.669 Seconds (without alignments) 3171.696 Million cell updates/sec Run on:

SEQ1-F 7276

1 MAWKTLPIYLLLLLSVFVIQ.....ARAITTRSGQTLSKVWYNCP 1363 score: Sequence: Title: Perfect :

BLOSUM62 Scoring table:

1356558 segs, 322682953 residues Gapop 10.0 , Gapext 0.1 Searched:

1356558

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

Published Applications AA:*

| cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/PCTUG_PUBCOMB.pep:*
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| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Semience 50 anni	Segmence 30 Appl	Semience 1 Appli	Segmence 2 Appli	, (2	1 4	֓֞֞֜֜֜֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֡֓֓֓֡֓֓֓֓֡֓֓֡֓			707	י י י	Segmence 30, Appr	ř (sednence 47, Appl	Sequence 104, App
	ID	US-10-124-557-52	US-09-802-207-30	US-09-897-188-1	US-10-124-557-2	US-10-124-557-62	US-10-124-557-46	US-10-124-557-60	US-10-124-557-40	US-10-124-557-142	US-10-124-557-48	US-10-124-557-50	US-10-124-557-44	TIC-10-104: EE7 40	74-100-47-01-00	US-10-124-557-104
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	Query Match Length DB	1363	1404	1404	1404	1404	1320	1320	1361	1313	1354	1314	1270	1311	1 .	1140
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	Score	7276	7261.9	7261.9	7261.9	7261.9	7058.7	7058.7	7044.6	7002	6987.9	6878.9	6794.7	6780.6		5820.9
	Result No.	П	2	3	4	S	9	7	8	σ	10	11	12	13		T-4

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3 US-10-124-557-18 3 US-10-124-557-18 3 US-10-124-557-18 3 US-09-802-207-27 4 US-10-124-557-6 3 US-10-124-557-6 3 US-10-124-557-6 3 US-10-124-557-6 4 US-09-922-217-10-124-557-6 5 US-10-124-557-6 5 US-10-124-557-6 5 US-10-124-557-6 5 US-10-124-557-6 5 US-09-922-217-10-124-557-7 5 US-10-124-557-7 5 US-10-124-557-7 6 US-09-921-217-10-124-557-7 7 US-09-801-388-10-124-557-7 8 US-10-124-557-7 9 US-10-124-557-7	3 US-10-124-557-72 4 US-10-243-243A-8 4 US-10-142-515-11 5 US-10-124-551-1 6 US-10-124-557-2 6 US-10-408-765A-2318 6 US-10-437-963-104793 4 US-10-146-473-50
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ALIGNMENTS

COMPUTATION ADDRESSES: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: CambridgePark Drive
CITY: Cambridge
STATE: 02140
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OVERALING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CIASSIFICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-DUN-1990
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-DUN-1990
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-GC-1989
APPLICATION NUMBER: US 07/57,196
FILING DATE: 29-GC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989 Sequence 52, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS: RESULT 1

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RESULT 2
US-09-802-207-30

i Sequence 30, Application US/09802207

j Publication No. US20020086824A1

j GENERAL INFORMATION:
   APPLICANT: Gerpten, John
   APPLICANT: Trent, John
   APPLICANT: John
   APPLICANT: Trent, John
   APPLICANT: John
   APPLICANT: Trent, John
   APPLICANT: John
   APPLICANT: Jo
                                                                                                                                                                                                                                                                                                                                         INPISRIABAMLQTITRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPD 1080
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                                                                                                                                                           ATTTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTEIMNKP
                                                                                                                                                                                                     901 ATTTEKTTESKITATTTQVTSTTTQDTTPFKLTTLKTTTLAPKVTTTKKTITTTEIMNKP
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Pred. No. 2.6e-167;
0; Mismatches 0;
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Matches 1363; Conserv
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                                                                                                                                                                                                                                                                                                                                                                          ; Score 7276; DB 13;
; Pred. No. 1.1e-167;
0; Mismatches 0;
                                                                                5190
                                                                                                                                                                                                                                                                                                             52:
                              NAME: CSETT, LUANN
REGISTRATION UNDBER: 31,822
REFERENCE/DOCKET NUMBER: GI 51
TELECOMMUNICATION INFORMATION:
TELEPONE: (617)876-1170
TELEFAX: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ. ID NO: 52:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                        DENGTH: 1363 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: US-10-124-557-52
              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1363; Conservative 0;
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Db 1141 DETNICNGKPUDGLTTLRNGTLYBFRGHYFWMLSPFSPESPARRITEVWGIPSPIDTVFT 1200 Oy 1160 RCNCEGKTFFFKDSOYMRFTNDIKDAGYPKPIFKGFGGLTGOIVAALSTAKYKNWPESVY 1219 Db 1201 RCNCEGKTFFFKDSOYMRFTNDIKDAGYPKPIFKGFGGLTGOIVAALSTAKYKNWPESVY 1260 OY 1220 FFKRGGSIQOYIYKQEPVQKCFGRRPALNYPVYGEMTQVRRRFFRRAIGPSOTHTIRIOY 1279 Db 1261 FFKRGGSIQOYIYKQEPVQKCFGRRPALNYPVYGEMTQVRRRFFRRAIGPSOTHTIRIOY 1279 Db 1261 FFKRGGSIQOYIYKQEPVQKCFGRRPALNYPVYGEMTQVRRRFFRRAIGPSOTHTIRIOY 1279 Db 1321 SPARLAYQDKGVLHNEVKVSILWRGLPNVYTSAISLPNIRKPDGYDYYAFSKDQYYNIDV 1339 Db 1331 SPARLAYQDKGVLHNEVKVSILWRGLPNVYTSAISLPNIRKPDGYDYYAFSKDQYYNIDV 1380 OY 1340 PSRTARAITTRSGCTLSKVWYNCP 1363 Db 1381 PSRTARAITTRSGCTLSKVWYNCP 1404	Sequence 1, Application US/09897188	Db 301 KEKITISAKETQSIEKTSAKDIAPISKVIARPIPKAFITIKGPALITPKEPTPITIRII
1 KRVCTAELS 1 KRVCTAELS 80 PPSGASCTI 21 PPSGASCTI 22 PPSGASCTI 23 PPSGASCTI 24 PPSGASCTI 24 PPSGASCTI 25 PPSGASCTI 26 PPSGASCTI 27 PPSGASCTI 26 PPSGASCTI 27 P	11 THE SEPTITIKE APTITIKE APTITITITITITITI APTITITITITITITI APTITITITITITITITITITITITITITITITITITITI	1040 OTPNSKIVEVNPKSEDAGGAEGETPHMILRPHVFMPBVTPDMDYLFRVPNQGIIINPMIS 1099 1081 OTPNSKIVEVNPKSEDAGGAEGETPHMILRPHVFMPEVTPDMDYLPRVPNQGIIINPMIS 1140 1100 DETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFT 1159

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Publication No. US20020137894A1
GENERAL INFORMATION:
    APPLICANT: Turner, Katherine
    APPLICANT: Turner, Stephen C.
    Jacobs, Kenneth
    Hewick, Rodney M.
    Gener, Thomas G.
    TITLE OF INVENTION: Megakaryocyte Stimulating Factors
    NUMBER OF SEQUENCES: 143
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                   APTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPBELAPTTPEEPTPTT
                       <u>АРТТТКЅАРТТРКЕРАРТТРККРАРТТРКВРАРТТРКЕРТРТТРКЕРАРТТКЕРАРТТРК</u>
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Version #1.25

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0,

ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive

CITY: Cambridge

STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02140 COMPUTER READABLE FORM:

APPLICATION NUMBER: US/10/124,557 FILING DATE: 16-Apr-2002 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989

5190

NAME: CSerr, Luann REGISTRATION NUMBER: 31,822 REFERENCE/DOCKET NUMBER: GI TELECOMMUNICATION INFORMATION:

ATTORNEY/AGENT INFORMATION:

TELEFACNE: (617)876-1170 TELEFAX: (617)876-5851

LENGTH: 1404 amino acids

1; 240 259 300 180 199 120 139 4 9 200 TOHNKUSTSPKITTAKPINPRPSLPPNSDISKETSLTVNKETTVETKETTTINKQTSTDG 241 TQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSDG 26 -----ELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP 61 KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP KIKSSKNSAANRELQKKLKVKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTST 1 MAWKTLPIYLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF PPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEEHSVSENQESSSSSSSSSSTIW Gaps Length 1404; 41; 0; Indels Query Match

99.8%; Score 7261.9; DB 13;
Best Local Similarity 97.1%; Pred. No. 2.6e-167;
Matches 1363; Conservative 0; Mismatches 0; Di 7 TOPOLOGY: linear ;
MOLECULE TYPE: protein ;
SEQUENCE DESCRIPTION: SEQ ID NO: US-10-124-557-2 1 MAWKTLPIYLLLLSVFVIQQVSSQ 80 121 140 181 d à

RESULT 4 US-10-124-557-2 ; Sequence 2, Application US/10124557

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Pred. No. 2.6e-167;
0; Mismatches 0; Indels 41;
                                                                                                                                                                                                                  Jacobs, Kenneth
Hewlick, Rodney M.
Gesner, Thomas G.
INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version
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APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION . cuhknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5190
                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62:
                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
PSRTARAITTRSGQTLSKVWYNCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAWKTLPIYLLLLSVFVIQQVSSQ
                                                                                                                       ; Sequence 62, Application US/10124557; Publication No. US20020137894A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : (617)876-1170
(617)876-5851
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                                                                                                                                                                            APPLICANT: Turner, Katherine Clark, Stephen C.
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                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Megak
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
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Best Local Similarity 97.1%;
Matches 1363; Conservative
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                                                                                     RESULT 5
US-10-124-557-62
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FFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRFERAIGPSQTHTIRIQY
                                                                            SPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYYAFSKDQYYNIDV
                                                                                                                                                                                                                                                                                     Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 7058.7; DB 13; Lengt
Pred. No. 2e-162;
0; Mismatches 0; Indels
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APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genetics Institute, Inc
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
                                                                                                                                        PSRTARAITTRSGOTLSKVWYNCP 1363
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                             RESULT 6
US-10-124-557-46
; Sequence 46, Application US/10124557
; Publication No. US20020137894A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
... APPLICANT: Turner, Katherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEFAX: (617)876-5851
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                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
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96.8%;
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Best Local Simi:
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                                     TQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTINKQTSTDG
                       KIKSSKNSAANRELQKKLKVKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTST
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61 SFCAEVHNPTSPPSSKKAPPPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEEHSVS 120	01 PALTTPKEPTPTTPKE 58 PALTTPKEPTPTTPKE 61 KEPAPTTPKEPAPTTT 18 KEPAPTTPKEPAPTTT 21 TTPKEPAPTTKEPAPT 79 TTPKEPAPTTKEPAPT 79 TTPKEPAPTTKEPAPT 79 TTPKEPAPTTKEPAPT 71 TTPKEPAPTTKEPAPT 71 TTPKEPAPTTKEPAPT	BI PARTITIXSAPTITIXEPARTITIXESAPTIENENE DELLI MARATITIXENE TELLE T	661 KETAPITIPKGTAPITIKKEAPKELAPITTKEPISTISKAPTTPKGTAPIT 720	901 ATTTEKTTESKITATTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTTAAPKWIKET 857 901 ATTTEKTTESKITATTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKTTTTTAAPKWIKET 857 901 ATTTEKTTESKITATTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKP 960 858 ATTTEKTTESKITATTTQVTSTTTQDTTPFKITTLLAFKVTTTKKTITTTEIMNKP 917 961 BETAKPKDRAINSKATTPKPQKPTKAPKKFTTTKKTTTTTAPKKMTSTMPE 1020 918 BETAKPKDRAINSKATTPKPQKPTKAPKKPTSTKKPKTTPTPFKKMTSTMPE 977 1021 LNPTSKIABAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPD 1080 978 LNPTSKIABAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPD 1037 1081 MDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSP 1140
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QY 1081 MDYLERVPNQGIIINEMLSDI Db 1038 MDYLERVPNQGIIINEMLSDI QY 1141 ARRITEVWGIPSPIDTVFTR QY 1201 QIVAALSTAKYKNWPESVYFR QY 1261 QIVAALSTAKYKNWPESVYFR Db 1158 QIVAALSTAKYKNWPESVYFR QY 1261 RRFEBAIGFSQTHTIRIQYSF QY 1261 RRFEBAIGFSQTHTIRIQYSF QY 1321 PDGYDYYAFSKDQYYNIDVPE QY 1321 PDGYDYYAFSKDQYYNIDVPE Db 1278 PDGYDYYAFSKDQYYNIDVPE	RESULT 8 US-10-124-557-40 Sequence 40, Application US/10124 Publication No. US20020137894A1 GENERAL INFORMATION: APPLICANT: Turner, Katheri APPLICANT: Turner, Katheri GLARK, Stephen Jacobs, Remeth Hewick, Redney GREENT: Turner, Renath Hewick, Rodney GREENT: ADDRESSE: STREET: 87 Cambridge I STREET: 87 CAMBRITE FORDW.	MEDIUM TYPE: Floppy d COMBUTER: IBM PC comp OPERATING SYSTEM: PC- SOFTWARE: PALENTIN PC- SOFTWARE: PALENTIN PALICATION DATA: APPLICATION NUMBER: U FILING DATE: 16-Apr- CLASSIFICATION DATA: APPLICATION NUMBER: U FILING DATE: 29-UN-1; FILING DATE: 29-UN-1; FILING DATE: 29-UN-1; FILING DATE: 29-DEC-1; FILING DATE: 29-DEC-1	APPLICATION NUMBER: UF FILING DATE: 08-AUG-1) ATTORNEY/AGENT INPORMATION NAME: CSETT, LUANN MAME: CSETT, LUANN BEFERENCE/DOCKET NUMBER: TELECOMMUNICATION INPORMATI TELEPHONE: (617)876-1877 INPORMATION FOR SEQ ID NO: 40: SEQUENCE CHRACTERISTICS: LENGTH: 1361 amino acid MOLECULE TYPE: amino acid MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ I
1 MAWKTLDIYLLLLSVPVIQOVSSQELSCKGRCFESFERCRECDCDAQCKKYDKCCPDYE 60 1 MAWKTLDIYLLLLSVPVIQOVSSQELSCKGRCFESFERCRECDCDAQCKKYDKCCPDYE 60 6 SFCAEVHNPTSPPSKRAPPSGASQTIKSTTKRSPRPPNKKYTKKVIESEBITEEHSVS 120 6 SFCAEVHNPTSPPSSKRAPPSGASQTIKSTTKRSPRPPNKKYTKKVIESEBITEEHSVS 120 6 SFCAEVHNPTSPPSSKRAPPSGASQTIKSTTKRSPRPPNKKYTKKVIESEBITE 115 121 ENQESSSSSSSSSTIWKIKSSKNSAANRELQKKLKVKDNKKNTTKKRPTPKPPVVDE 180 116	PALTIPKE PALTIPKE KEPAPTIE TIPKEPAP TIP	601 PITPEELAPTTPEEPAPTTPKAAANTPKEPAPTTPKEPAPTTP 660 558 PITPEELAPTTPEEPTTPEEPAPTTPKAAANTPKEPAPTTP 661 558 PITPEELAPTTPEEPTTPEEPAPTTPKAAANTPKEPAPTTPKEPAPTTP 617 661 KETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTT 720 618 KETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTT 677 721 PKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPT 780 678 PKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPT 737 781 TPKETAPTTPKEPAPTTPKKPAPTTLKEPAPTTSKSVSTPTTHKKSPDESTPELS 840 781 TPKETAPTTPKEPAPTTPKKPAPTTSKSVSTPTTTKEPTTHKKSPDESTPELS 737 781 TPKETAPTTPKEPAPTTPKKPAPTTSEVSTPTTKEPTTHKKSPDESTPELS 797	841 AEPTPKALENSPKEPGVPTTKTPAATKPEMITTAKDKTTERDLATTAAPKMTKET 900 798 AEPTPKALENSPKEPGVPTTKTPAATKPEMITTAKDKTTERDLATTAAPKMTKET 957 901 ATTTEKTTESKITATTTGVTSTTTGDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKP 960 858 ATTTEKTTESKITATTTGVTSTTTGDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKP 917 961 BETAKPKDRAINSKATTPKPGVFTAPKRTKKTTTLAPKVTTTKKTITTTFIMNKP 917 961 BETAKPKDRAINSKATTPKPGVFTKAPKKPTKTKKTTTTAPKVTTSTMPE 1020 918 BETAKPKDRAINSKATTPKPGKPTKAPKKPTSTKKPKTTTPTPRKGTTSTMPE 977 1021 LNPTSRIABAMLGTTTRPNGTPNSKLVEVNPKSEDAGGAGGETPHMLLRPHVFMPEVTPD 1080 978 LNPTSRIABAMLGTTTRPNGTPNSKLVEVNPKSEDAGGAGGETPHMLLRPHVFMPEVTPD 1037
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22 980 24 978 25 1040 26 1038 27 1100 28 1098 28 1160 29 1158 29 11280 20 1280	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/124,557 FILING DATE: 16-Apr-2002 CLASSIFTCATION: CURKNOW: PRIOR APPLICATION NUMBER: US 07/643,502 FILING DATE: 18-JAN-1991 APPLICATION NUMBER: US 07/643,502 FILING DATE: 18-JAN-1991 APPLICATION NUMBER: US 07/546,114 FILING DATE: 29-UNN-1990 APPLICATION NUMBER: US 07/390,901 FILING DATE: 29-DEC-1989 APPLICATION NUMBER: US 07/390,901 FILING DATE: 08-AUG-1989 APPLICATION NUMBER: 31,822 RESERRENGE/DOCKET NUMBER: GI 5190 TELECOMMUNICATION INDREMER: GI 5190 TELECOMMUNICATION INDREMER: GI 5190 TELECOMMUNICATION INDREMER: GI 5190 TELECOMMUNICATION INDREMER: GI 5190 TELECOMMUNICATION INDEMATION: TELECOMMUNICATION INDREMER: GI 5190 TELECOMMUNICATION INDREMATION: TELECOMMUNICATION INDREMATION: TELECOMMUNICATION INDEMATION:
Duery Match Best Local Similarity 94.04; Pred No. 4.59-163; Length 1361; Best Local Similarity 94.04; Pred No. 4.59-163; Matches 1320; Conservative 0. Mismacches 0; Indels 84; Gaps 2; 1 MARKTIPILILIS/PULDUSSSQ	APTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKG APTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKG APTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKG TAPTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPK TAPTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPK KPAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPK TAPTLKEPAPTTPKEPTTTKEPTTTHKSPDESTPELSAEPTPKALENSPKEPGVPT TKPAATKPEMTTTAKDKTTREDLRTTPETTTAAPKMTKETATTTEKTTTTTOV TKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTTTTTTT TKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTTTTTTTTT TKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTTTTTTTTTTTTTTTTTTTTTTTTTTT

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                                                               961 EETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPE
                                                                                911 EETAKPKDRATNSKATTPRPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPE
                                                                                                                               LNPTSRIABAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPD
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US-10-124-557-48

Sequence 48, Application US/10124557

Publication No. US20020137894A1

GENERAL INFORMATION:
HORITORY: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gener, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143

CORRESPONDENCE ADDRESS:
STRATE: Massachusetts

STATE: Massachusetts
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ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CLASSIFICATION INDRER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION INDRER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-DEC-1889
APTICATION NUMBER: US 07/457,196
FILING DATE: 08-AUG-1889
ATTORNEY AGENT INFORMATION:
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REGISTRATION NUMBER: 31,822
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                                                                                                                                                   Length 1313;
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                                                                                                                                                    Score 7002; DB 13;
Pred. No. 4.5e-161;
0; Mismatches 0;
                 INFORMATION FOR SEQ ID NO: 142:
                                                                                                                                                    Query Match
Best Local Similarity 96.3%;
Matches 1313; Conservative
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                                                                                      POKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPN
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: OF COMPATIBLE PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: IG-Apr-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating I
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FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
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STATE: Massachusetts
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                              Score 6987.9; DB
Pred. No. 1e-160;
0; Mismatches (
   5190
                                                                                           TYPE: amino acid

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 48:
 IJ
      TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 1354 amino acids
                                                                                                                                                                                                                                                       1 MAWKTLPIYLLLLSVFVIQQVSSQ
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                              96.0%;
                                                                                                                                                                                                       Best Local Similarity 93.5
Matches 1313; Conservative
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STATE: Massachusetts
COUNTRY: U.S.A.
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Pred. No. 4.3e-158;
7; Mismatches 14;
    FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                   5190
                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
                                                                     NEI/ANGERT LUADD
NAME: CSerr, LUADD
REGISTRATION NUMBER: 31,822
                                                                                                  REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INDORMATION:
TELEPHONE: (617)876-1170
TELEPAX: (617)876-5851
                                                                                                                                                  INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 1314 amino acids
                                                                                                                                                                                                                                                       vuery match 94.5%;
Best Local Similarity 94.7%;
Matches 1292; Conservative 7
                                                                                                                                                                                      TYPE: amino acid
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Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hawick, Rodney M.
Gener, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143 Version #1.25 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/124,557 FILING DATE: 16-Apr-2002 CLASSIFICATION: <UNKNOWN>

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          KETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTT
                                                                              PKEPAPTIPKEPAPTIPKGTAPTILKEPAPTIPKKPAPKELAPTITKGPISTISDKPAPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: FOPOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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STREET: 87 CambridgePark Drive
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STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                             Query Match 93.4%; Score 6794.7; DB 13; Lengt Best Local Similarity 93.2%; Pred. No. 4.4e-156; Matches 1270; Conservative 0; Mismatches 0; Indels
          APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PEDLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-124-557-44
                                                                                                                   NAME: CSGIT, LABOR
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET UNMBER: GI 57
REPERCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617)876-1170
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1270 amino acids
                                                                                                            ATTORNEY/AGENT INFORMATION:
 APPLICATION DATA:
                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
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PRIOR
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APTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTT
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Publication No. US20020137894A1

GENERAL INFORMATION: Katherine
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Renneth
Hewalck, Rodney M.
Genner, Thomas G.

TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143

CORRESPONDENCE ADDRESS:
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STREET: 87 CambridgePark Drive
CITY: Cambridge
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Pred. No. 1e-155;
0; Mismatches 0; Indels
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                                   FILING DATE: 16-Apr-2002

FLING APPLICATION: «Unknown»

PRIOR APPLICATION NOTABER: US 07/643,502

FILING DATE: 18-JAN-1991

APPLICATION NUMBER: US 07/546,114

APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-JUN-1990

APPLICATION NUMBER: US 07/457,196

FILING DATE: 29-DEC-1989

APPLICATION NUMBER: US 07/390,901

FILING DATE: 08-AUG-1989

APTORNEY/AGENT INFORMATION:
             NT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
                                                                                                                                                                                                                                    5190
                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-124-557-42
                                                                                                                                                                                                          NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAWKTLPIYLLLLLSVFVIQQVSSQ-
                                                                                                                                                                                                                                                                                                                        LENGTH: 1311 amino acids
                                                                                                                                                                                                                                                                TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                               TELEFAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                       93.2%;
90.5%;
                                                                                                                                                                                                                                                                                            OR SEQ ID NO: 42:
CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                             INFORMATION FOR
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                            TTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKP
                                                                                               TIKSAPITPKEPSPITIKEPAPITPKEPAPITPKKPAPITPKEPAPITPKEPAPITIKK
                                                                                                                              560 APTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEBLAPTTPEEPTPTT
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Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARRE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-124-557-58
Sequence 58, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAWKTEPIYLLILLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----ELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP
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                                                                                                         Version #1.25
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80.0%; Score 5820.9; DB 13
Best Local Similarity 96.4%; Pred. No. 1.3e-132;
Matches 1099; Conservative 0; Mismatches 0;
                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: CURROWN.>
PRIOR APPLICATION DATA:
                                                                                                                                                                                       APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
                                                                                                                                                                                                                                                                                                                                NAME: CSEXY, LUANN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAWKTLPIYLLLLLSVFVIQQVSSQ-
                                                                                                                                                                                                                                                                                                                                                                                                             (617)876-5851
Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 104
SEQUENCE CHARACTERISTICS:
                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1140 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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KETAPTTPKGTAPTTLKEPAPTTPKKPAPKBLAPTTTKEPTSTTSDKPAPTTPKGTAPTT
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                                                                                                                                                                                                                                                                                                      Length 1049;
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                                                                                                                                                                                                                                                                                                    76.4%; Score 5561; DB 13;
95.5%; Pred. No. 2.2e-126;
cive 0; Mismatches 0;
         OR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-URN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1899
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                          NAME: CSETI, LUANN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-124-557-58
                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 1049 amino acids
                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                    TYPE: amino acid
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Best Local Similarity 95.5
Matches 1049; Conservative
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1020 1080 1030 960 850 **BETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPPTPRKMTSTMP**E 911 BETAKEKDRATHSKATTERREQKETKAPKKETSTKKERTHMERVRKEKTTETERKMTSTMEE AEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKET AEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRITPETTTAAPKMTKET ATTTEKTTESKITATTTQVTSTTTQDTTPFKLTTLKTTTLAPKVTTTKKTLTTTEIMNKP LNPTSRIABAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPD **TPKETAPTTPKKEPAPTTPETPPPTTTSEVSTPTTTKEPTTIHKSPDESTPELS** PKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPT 1031 MDYLPRVPNQGIIINPMLS 1049 MDYLPRVPNQGIIINPMLS 1099

October 13, 2004, 11:53:15

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

October 13, 2004, 11:23:49 ; Search time 149.862 Seconds (without alignments) 5233.063 Million cell updates/sec Run on:

SEQ1-F 1276 1 MAWKTLPIYLLLLSVFVIQ.....ARAITTRSGQTLSKVWYNCP 1363 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.1

1825181 seqs, 575374646 residues Searched:

Total number of hits satisfying chosen parameters:

1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	-	Description	Ogoga Andrew	0 0 0	101	IOIIIO SADI	1 5	mus muscu		n t	O7k+fc drocontil	Appendig dropping		nomo sapie		Vessee cnlamydomon	Adsu/044 Chlamydom	QU6852 Clostridium	Wedgis bos taurus	Aas83977 bos tauru	Vesses chlamydomon	Adsu/042 chlamydom	V/Ktps drosophila	Adulussi drosophil				Conces House appear		caenornab	Yordie dicsopnila		O9vpql drosophila	
SUMMARIES	<u>-</u>	i	092954	Q9BX49	06ZMZ5	BAD18580		077765	09VR49	MUC2 HUMAN	O7KTF6	AAS64673		CAPMINS	2000 2000 2000 2000 2000 2000 2000 200	AAS07044	н.	11/1	A B C 8 3 9 7 7		A B S 0 7 0 4 2		AANTOSST		OBIRSS	O8WWO4	MUSB HUMAN	076894	098487	081018	AAN10358)	Q9VPG1	
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P70670 mus musculu Q10465 homo sapien Q7qkk7 anopheles q	Q8isf5 caenorhabdi Q8isf6 caenorhabdi Q8isf7 caenorhabdi	29.42.3 drosophila 29.42.3 drosophila 28.645 phytophthor Aap7.4661 phytophth	Q2000) Caenorhabdı O96449 phytophthor Q91ie8 arabidopsis Q9w3z0 drosophila
P70670 Q10465 Q7QKK7	Q8ISF5 Q8ISF6 Q8ISF7 O9VEL9	09W2Z3 Q8H6Q5 AAP74661	Q9W3Z0
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2187 7962 972	10578 18519 18534 2112	4498 1607 1607	1489 1480 3166
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1065.3 1061.4 1028	1027.2 1027.2 1027.2 1024.8	1024.2 1024 1024 1023.2	1020.2 1018.6 1018.6
0 0 0 0 0 4 4 1	337 337	8 4 4 4 8 0 1 2	4 4 4 4 5

ALIGNMENTS

RESULT 1 Q92954 D Q92954 PRELIMINARY; PRT; 1404 AA.	01-FEB-1997 (TrEMBLrel. 02, Creat		Megakaryocyte stimulating factor.	Eukaryota: Metazoa: Chordata: Craniata: Vortokunta		NCB1_TaxID=9606; [1]			Nellener K., Glannotti J., Calvetti J., Fitzgerald M., K. Perenz C., Grobholz J., Fraser H., Besh V., Mouton J.	Bhatia S., Kriz R., Hewick R., Clark S.C.,					Merberg D.M., Fitz L.J., Temple D. Giennotti T. M. L.L.		Jacobs K., Turner K.;		(in) Freissner K.T., Rosenblatt S., Kost C., Wegerhoff J., Mosher D.F. (eds.):		Science Publishers B.V. (1993).		SEQUENCE FROM N.A.	Kelleher K. Gjannotti I Calwetti I Eitzensta W.	Ferenz C., Grobholz J., Fraser H.,	Bhatia S., Kriz R., Hewick R., Clan								PR00022; SOMATOMEDINE.	SMART; SM00120; HX; 2.	ភិ ្	2 23		
R O L A	占	H	OE	88	80	R C	RP	R E	\$ \$	RA F	T E	RT	R.	X G	2	RA	RA E	χ t	집원	RL	3.5	Z 5	አ ካ 4	£ 5	R.	₹ E	Z K	DR	H I	E 5	i ii	DR	DR	DR	¥ 5	Z Z	DR.	S S	

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PPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEEHSVENQESSSSSSSSSSTIW 139
                                                                                                                                                                       SPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYYAFSKDQYYNIDV 1339
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                                OTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLS
                                              DETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFT
                                                                                                                   RCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVY
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1404;
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A Wray P.;

B Wray P.;

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AL13355; CAC36090.1; -.

R HSSP; P04004; 10C0.

R InterPro; IPR001212; Somatomedin_B.

R InterPro; IPR001212; Somatomedin_B.

R Pfam; PF010045; Hemopexin; 2.

R Pfam; PF010133; Somatomedin_B; 2.

R Pfam; PR00122; SOMATOMEDINB.

R SMART; SM00120; MX; 2.

R SMART; SM001201; SO; 2.

R SMART; SM001201; SO; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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PROSITE; PS00524; SOMATOMEDIN B; 2.
SEQUENCE 1404 AA; 151076 MW; 782A11746B3FDEE5 CRC64;
                                                                                                                                                                                                                                                                                                                           Q9BX49 PRELIMINARY; PRT; 1404 AA.
Q9BX49;
01-UNN-2001 (TrEMBLrel. 17, Created)
01-UNN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
BG17416.2 (MSF: megakaryocyte stimulating factor ).
Name=bG17416.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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Pred. No. 1.1e-140;
0; Mismatches 4;
                                                                                                                                                                                                                                                  PSRTARAITTRSGOTLSKVWYNCP 1363
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Mammalia; Eutheria; Primates;
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96.8%;
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                                                                   Gaps
                                 41;
          Length 1404;
                                 Indels
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              7261.9; DB 2
No. 2.7e-141;
             DB
                                  0; Mismatches
              Score '
Pred. 1
                                                      1 MAWKTIPIYLLLLLSVFVIQOVSSQ-
             Query Match 99.8%;
Best Local Similarity 97.1%;
Matches 1363; Conservative
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140 KIKSSKNSAANRELOKKIKVKONKKARTKKKPTPREPVVDEAGSGLDNGPFKVTTPDTST 199	320 TIPRESPECTIVES PRINCES PATTICES PAT

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	BAD18580 ID BAD18580 PRELIMINARY; PRT; 933 . AC RAD18580;	DT 12-MAY-2004 (TrEMBLrel. 27, Created) DT 12-MAY-2004 (TrEMBLrel. 27, Last sequence DT 12-MAY-2004 (TREMBLrel. 27, Last annotation	DE CUDA FULIDOSOI ILS, CIOURO DE SADIOR STOCKOOT SE SADIORS DE SADIORS DE SUDETÍCIAL ZONE, DECORE, CAMPLODACETY,	DE pericarditis syndrome) (FKG4). OS Homo sapiens (Human). OC Bukaryota; Metazoa; Chordata; Craniata; V	Mammaila; butheria; Filmates; NCBI_TaxID=9606; [1]		RA Ota I., Nakagawa S., Senon A., Mizugucui. RA Irie R., Otsuki T., Sato H., Wakamatsu A.	RA Isono Y., Kawai-Hio Y., Salto K., Mismissa RA Yamashita H., Matsuo K., Nakamura Y., Sek	RA Wagarbuma M., Muraxama B., Suzuki Y., Suga RA Sugiyama A., Kawakami B., Suzuki Y., Suga RA, Masuho Y., Nagai K., Isogai T.,	RT "NEDO human cDNA sequencing project."; RL Submitted (MAR-2004) to the EMBL/GenBank/		หะ	Matches 931	H 19	DP 61 SFCAEVHNPTSPPSSKKAPPPSGASQTIKST	121	Db 121 ENGESSSSSSSSSSSTIRKIKSSKNSAANR	OY 181 AGSGLDNGDFKVTTPDTSTTQHNKVSTSPKI'	Db 181 AGSGLDNGDFKVTTFDTSTTQHNKVSTSFKL1 Ov 241 TTVETKETTTTNKQTSTDGKEKTTSAKETQS	241	Qy 301 PALTTPKEPTPTTPKEPASTTPKEPTPTIK	DD 301 PALTTPKEPTPTTPKEPASTTPKEPTPTTK	Oy 361 KEPAPTTPKEPAPTTTKEPAPTTTKSAPTTP	Db 361 KBPAPTTPKE			(y 481 PARTIINSARTIINSFRITTINSTITTINS		371
		KEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTP 42 KRPAPTTPKE37	TTPKEBARTTKEPARTTPKEPARTARKKPARTTPKERARTTPKEBARTTTKEPSPTTPKE 48	PAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKKPAPTTP		KEPAPITEKEPAPITIKKPAPIAPKEPAPITPKETAPITTPKKLTPITPEKLAPITPEKPA		PITPEBLAPITPEBPIPTIPEEPAPITPKAAAPNIPKEPAPITPKEPAPITPKEPAPITP 66	37	KETAPITPROJAPITUMBPAPITENNERGEBERT	PKEPAPITTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPT 78		IPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELS 84	 ABPTFKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLKTTPETTTAAPKMTKET	AEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTTERDLKTTPEITTAAFKNTKEI AEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTTER	ATTEKTTESKITATTOVISTTOOTSFKITLIKITLARKOTILALIANAA 	BETAKEKDRATUSKATTPKPOKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPE 102		INPTSRIABAMLOTTTRPNOTPNSKLVBVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPD	INPTSRIAEAMLQTTTRPNQTENSKLVEVNPROSDJAGGAEGE FRANLLAFTEN FOR EN ANTER MANTED VIDOV TOTANDALISTER SPENDEN STANLED FROM SPENDEN SPENDE SPENDEN SPEND SPENDEN SPEND SPENDEN SPEND	MDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPFSP 71	ARRITEVWGIPSPIDTVFTRCNCEGKTFFFKDSQXWRFTNDIKDAGYPKPIFKGFGGLTG 120	ARRITEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTG	QIVAALSTAKKKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRR		RRFERAIGPSQTHTIRIQYSPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRK 132	SLPNVYTSAISLPNIRK 8	PDGYDYYAFSKDQYYNIDVPSRTARAITTRSGQILSKVWINCE	,

CITARRINPRESEPRNSDISKETSLIVNKE 240 KSAPTTPKEPAPTTTKSAPTTPKEPAPTTT 360 ттркетарттрккітрттрекцарттрекра 600 TTKRSPKPPNKKKTKKVIESEEITEEHSVS 120 PKEPAPTTPKKPAPTTPKEPAPTTPKEPTP 420 370 APTIPKEPAPTIPKEPAPTITKEPSPITPKE 480 EPSPITIKEPAPITPKEPAPITPKKPAPITP 540 RELOKKIKVKDNKKNRTKKKPTPKPPVVDE 180 GRCFESFERGRECDCDAQCKKYDKCCPDYE 60 chi H., Inagaki H., Sugiyama T., u A., Ishii S., Yamamoto J., hikawa T., Kimura K., Sekine M., Kikuchi H., Kanda K., ., Takahashi-Fujii A., Oshima A., Sugano S., Nagahari K., GRCFESFERGRECDCDAQCKKYDKCCPDYE ; DB 2; Length 933; 6.1e-92; hes 2; Indels 430; Gaps ce update)
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noderately similar to Homo
selmularing factor, arricular
arthropathy, coxa vara, Vertebrata; Euteleostomi; i; Hominidae; Homo. k/DDBJ databases. C5BC21A23 CRC64;

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                                  HSSP; P04004; 10C0.

R MGD; MGI:1891344; Prg4.

R InterPro; IPR001212; Somatomedin_B.

R Ffam; PF00045; Hemopexin; 2.

R Ffam; PF00033; SOMATOMEDINB; 2.

R PRINTS; PR00021; SOMATOMEDINB.

R SMART; SM00120; HX; 2.

SMART; SM00120; HX; 2.

R PROSITE; PS00024; HEMOPEXIN; UNKNOWN 1.

R PROSITE; PS00524; SOMATOMEDIN B; 2.

R PROSITE; PS00524; AMATOMEDIN B; 2.

SEQUENCE 1054 AA; 115991 MW; 4FC64BFA42283235 CRC64;
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Matches 769; Conservative
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Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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"Isolation, characterization and mapping of the mouse and human (proteoglycan 4) genes.";
Cytogenet. Cell Genet. 90:291-297(2000).
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MEDLINE=20573856; PubMed=11124536;
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                                                                                                                                                                                                                                                                                       RRFERAIGPSQTHTIRIQYS-PARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIR
                                                                                                                                                                                                 PKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALE
                                                     NSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTE
                                                                                                SKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTBIMNKPEETAKPKDR
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Immunodetection and partial cDNA sequence of the proteoglycan,
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MEDLINE-99171663; PubMed-10073655;
Schumacher B.L., Hughes C.E., Kuettner K.E., Caterson B.,
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26, Last annotation update)
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Bos taurus (Bovine).
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01-MAR-2004
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MEDLINE-ZOUGHORG, PubMed=10731132;

MEDLINE-ZOUGHORG, S. Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Kichtards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
An K.H., Doyle C., Baxer B.G., Halt G., Nelson C.R., Gabor G.L.,
Abril J.F., Agbayani A., An H.J., Bayraktaroglu L., Bashey E.M.,
Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Abrill W.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1205 ALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 ALSIAQYKSRPESVYFFKRGGSVQQYTYKQEPTQKCTGRRPAINYSVYGETAQVRRRRFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1085 PRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPARRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               966 PKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRK-MTSTMPBLNPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                       3;
superficial zone protein, synthesized by cells lining synovial
                                                                                                                                                                                                                                                                                                                   DB 2; Length 401;
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
fri TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                          52; Indels
                                                                                                                                                                                                                                                           401 AA; 44952 MW; 86147CC9AFBB73D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DYYAFSKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP 1363
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Last annotation update)
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Pred. No. 6e-28;
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                                        joints.";
Joints.";
Joints.";
J. Orthop. Res. 17:110-120(1999).
EMBL; AF056218; AAD13404.1; -.
InterPro; IPR000585; Hemopexin.
Pfam; PF00045; Hemopexin; 2.
SMART; SM00120; HX; 2.
PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
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80.2%;
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01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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1264

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de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Ra Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

Burbin K.J., Evangelista C.C., Ferriaz C., Ferriera S., Fleischmann W.,

Ra Glodek A., Gong F., Garg N.S., Gelbart W.M., Glasser K.,

Ra Hortis N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

Ra Hostin D., Houston K.A., Howland T.J., Wein M.H., Ibegwam C.,

Ra Jali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Rak Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Lasko P., Lei Y., Levtsky A.A., Li J., Li Z., Liang Y., Lin X.,

Ra Lasko P., Lei Y., Levtsky A.A., Li J., Li Z., Liang Y., Lin X.,

Ra Lasko P., Lei Y., Levtsky A.A., Li J., Li Z., Liang Y., Lin X.,

Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Ra Reinert K., Remington K., Sunders R.D., Scheeler F., Shen H.,

Ra Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

Spier E., Spradling A.C., Stapleron M., Strong R., Sun E.,

Syler E., Spradling A.C., Stapleron M., Strong R., Sun E.,

Ray Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhang L.,

Ray Rein S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

Ray Syliskas R., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

Ray Shier E., Spradling R.C., Turner R., Venter J.C.,

Ray Shier S.M., Moodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

Ray Shier S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

Ray Shier S.M., Woodager, Worley W., Zhou X., Zhou X., Smith H.O.,

Ray Shier S.M., Woodager, Worley W., Zhou X., Zhou X., Smith H.O.,

Ray Shier S.M., Woodager, Worley W., Zhou X., Zhou X., Smith H.O.,

Ray Shier S.M., Woodager, W., Rubin G.M., Venter J.C.;

Ray Solone Sequence of Drosophila melanogaster.",
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SEQUENCE FROM N.A.
MEDLINE-22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Syirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22426065; PubMed=12537568; Calniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Ffeifer B.D., Richards S., Sodergren E.J., Raches R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Nyers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: release 3 of the Drosophila Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-22426069; PubMed=12537572; Matthews B.B., Campbell K.S., Hraddcky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lewis S.E.; "Annotation of the Drosophila melanogaster euchromatic genome:
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EMBL, AE003575, AAF50957.3; -.
FlyBase; FBgn0003372; Sgsl.
SEQUENCE 1225 AA; 127735 MW; A99AF9D4404C79F4 CRC64;
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                RAPARA RA
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DB 2; Length 1225;

Score 1384.6;

19.08;

Query Match

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214
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                                                  ----SQEL--SCKGRCFESFERGRECDCDAQCKKYD
                       Gaps
                                                                                                       KCCPDYESFCAEVHNPTSPPSSKKAPPPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEI
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                                                                                                                                                                                                    ------TKRTTKRTTRRPTT
                                                                                                                                                                                                                                    STTQHNKVS----TSPKITTA
                                                                                                                                                                                                                                                  165 PPCT------CŚBESSTAIPSSPCIDISTVIPISPCTQETTTPPPTCŚTQGTQTTP
                                                                                                                                                                                                                                                                                                                                                                                                           TPKEPTPTTIKSAPTTPKEPAPTTTKSAP--TTPKEPAPTTTKEPAPTTPKEPAPTTKE
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                  Mismatches 428;
       3.2e-20;
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    Pred. No.
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                  135;
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   25.1%;
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Best Local Similarity
Matches 378; Conser
                 378;
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 915 PRSTTTTCTSGPTT--TTPRSTTKTSTCAPT----TTTPRSTTTTTSTSRPTTTTPRSTTT 968
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                       874 AKDKITERDLRITIPETITAAPKMIKETAITIEKITESKITAITIQVISITIQDITPFKII
                                                                                                            ---KPTSTKKPKTMPRVRKPKTTPTPRKMT----STMPELNPTSRIAEAMLQTTTR----
                                                                                                                           MEDLINE-94132002; PubMed-8300571; Gum J.R. Jr., Hicks J.W., Toribara N.W., Siddiki B., Kim Y.S.; Gum J.R. Jr., Hicks J.W., Toribara N.W., Siddiki B., Kim Y.S.; "Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of the amino terminus and overall sequence similarity to prepro-von Willebrand factor.", J. Biol. Chem. 269:2440-2446(1994).
                                         969 T---TISRPTITIPRSTI-----TASTSRPTITIPRSTI----
                                                                  934 ILKTITLAPKVITIKKTITITEIMNKPEETAKPKDRAINSKAITPKPQKPIKAPK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91358717; PubMed=1885763;
Toribara N.W., Gum J.R. Jr., Culhane P.J., Lagace R.E., Hicks J.W.,
Petersen G.M., Kim Y.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human small intestinal mucin gene structure. Repeated arrays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gum J.R. Jr., Hicks J.W., Toribara N.W., Rothe E.-M., Lagace R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                              1119 CHPQPPYQIPPWSWWYPNPTYPNPVWPWQPN-----
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Name=MUC2; Synonyms=SMUC;
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MEDLINE=93016075; PubMed=1400449;
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MUC2 HUMAN Sirm.-
QO28I7; Q14878;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Entropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                             SUBUNIT: Multimeric.

-: SUBUNIT: Multimeric.
-: SUBCELJULAR LOCATION: Secreted.
-: SUBCELJULAR LOCATION: Secreted.
-: SUBCELJULAR LOCATION: Secreted.
-: TISSUE SPECIFICITY: Colon, small intestine, colonic tumors, bronchus, cervix and gall bladder.
-: PTM: All cysteine residues are involved in intrachain or interchain disulfide bonds (By similarity).
-: POLYMORPHISM: The number of repeats is highly polymorphic and varies among different alleles.
-: SIMILARITY: Contains 1 Cterminal cystine knot-like (CTCK) domain.
-: SIMILARITY: Contains 2 VWFC domains.
       J. Clin. Invest. 88:1005-101311991).
-!-FUNCTION: Coats the epithelia of the intestines, airways, and other mucus membrane-containing organs. Thought to provide a protective, lubricating barrier against particles and infectious agents at mucosal surfaces.
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PROSITE; PS01225; CTCK 2; 1.
PROSITE; PS01022; EGF 1; UNKNOWN 1.
PROSITE; PS01030; VWFC 1; 2.
Glycoprotein; Repeat; Signal.
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InterPro; IPR002209; Cysrich TIL.
InterPro; IPR002209; Cysrich TIL.
InterPro; IPR002209; Cys knot.
InterPro; IPR006209; EGF like.
InterPro; IPR001009; WPF_C.
InterPro; IPR001046; WWF_C.
InterPro; IPR001046; WWF_C.
IPEam; PF00009; Cys knot; 1.
Pfam; PF00093; WWC; 1.
Pfam; PF00094; WWC; 1.
SWART; SM00041; CT; 1.
SWART; SM00214; WWC; 2.
SWART; SM00214; WWC; 2.
Clin. Invest. 88:1005-1013(1991).
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EMBL; M94131; AAA59163.1; -.
EMBL; M94132; AAA59164.1; -.
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Genew; HGNC:7512; MUC2.
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REPEINEE FOLLOGOUNG, PubMed=10731132;

RADINE=20196006, PubMed=10731132;

RADINE=20196006, PubMed=10731132;

RADINEE S.E., In P.W., Hookins R.A., Galle R.F.,

RADINEE R.A.

REPEINEE R.G., Rogers Y.E.,

RADINEER R.G., Champe M., Pfeitfer B.D.,

RADINEER R.G., Rogers Y.E.,

RADINEER R.G., Champe M., Pfeitfer B.D.,

RADINER R.M., Basu A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RADINER R.M., Basu A., Barch R.G., Champe M., Pfeitfer B.D.,

RADINER R.M., Basu A., Barch R.G., Champe N., Bolck G.L.,

RADINER R.M., Barner B.P., Butler P., Cadieu E., Canter A., Chandra I.,

RADINER R.M., Barner R.G., Butler R., Cadieu E., Canter A., Chandra I.,

RADINER R.D., Butler R., Cadieu E., Control R.C., Dunn P.,

RADINER R.D., Butler R., Down B.C., Dunn P.,

RADINER R., Butler R., Carpan R.C., Perriac S., Fleischmann W.,

RADINER R., Brangelista C.C., Perriac S., Fleischmann W.,

RADINER R., Gorrell J.H., Gal Z., Glan P., Harris M.,

Harris N.L., Harvey D., Heiman T.J., Harris M.,

RADINER R., Kalubh F., Karpen G.H., Kee Z., Kannison J.A., Liai Z.,

RADIN R., Matlan R.C., Karait C., Kravitz S., Kulp D., Lai Z.,

RADIN R., Matlan R.C., Karait C., Remison J.A., Liai Z.,

RADIN R., Matlan R.C., Romer R.C., Morris J., Moshrefi A.,

RADIN R., Matleri B., McIntosky A.A., Li J., Li Z., Liang Y., Lin X.,

RADIN R., Matlan R.D., Mourphy B., Murphy L., Moshrefi A.,

RADIN S.M. Mount S.M., Moy M., Murphy B., Murphy L., Pacleb J.M.,

RADIN R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RADIN R., Relson R.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RADING S.M., Moy M., Murphy R., Nusskern D.R., Pacleb J.M.,
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                                      ---KPQKPTKAP-----KKPTSTKKPKTMPRVRKPKTTPTPRKMTSTM
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--GVPT-TKTPAATKPEMTTTAKDKTTERDLR---TTP--ETTTAAPKMT---KETATTT
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Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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91; 143 --PDT 197 ------TKKSTTLRTEEPTTRKSST 191 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Smith T., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao G., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Glbbs R.A., Wyers B.W., Rubin G.M., Venter J.C.; The genome sequence of Drosophila melanogaster."; 47 AQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAPPPSGASQTIKSTTKRSPKPPNKKKTKK Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise B., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin: ---SSSSSTIWKI----KS 881; Gaps MEDLINE=22426069; PubMed=12537572;
MiSEAS. Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Miscas S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.,
Bradecky P., Huang Y., Kananker J.S., Millburn G.H., Perchnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
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Bartaris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
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MEDINE 22426065.

Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A. Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Stacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Wyers E.W., Gibbs R.A., Rubin G.M., Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.";

Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002). DB 2; Length 1761; "Annotation of the Drosophila melanogaster euchromatic genome: 144 SKNSAANRELOKKLKVKDNKKNRTKKKPTPRPPVVDEAGSGLDNGDFKVTT-Indels 1761 AA; 197521 MW; 62A5E16E6241B3F4 CRC64; to the EMBL/GenBank/DDBJ databases. Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases. 472; Conservative 117; Mismatches 400; a genomics perspective."; Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002). Score 1349.9; DB Pred. No. 3.3e-19; Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002). 107 VIESEEITEEHSVSE--NQESSSSSSS----------THNHL-----MEDLINE=22426070; PubMed=12537573; EMBL; AE003626; AAS64673.1; -. InterPro; IPR011009; Kinase_like. 18.6%; 25.2%; Submitted (SEP-2002) review."; Query Match Best Local Similarity SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. 161 AETKK--Lewis S.E.; systematic NON TER SEQUENCE FLYBASE; FLYBASE; Matches g ð g

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_	QY 874 AKDKITERDLR	895	Db 1385 STTKTTREPTTKRVTTERTTR	OY 940 LAPKVITIK Db 1443 LKPTEEPTTRKTGFTFEP	Qy 978 PKPOKP	1503	Qy 992STKKPKTM	Db 1563 TKKTTTKKTTHEPTTKKSTTL	QY 1036TRPNQTPNSKLVI Db 1619 TTKRTTABMSTTNQEPTSVET	Qy 1073 FMPEVTPDMDYLPRVPNQGII	Db 1676 LGPSILPLPDLP	1133 SPFSPPSPARRITE	1688	OY 1193 KGFGGLTGQIVAALSTAKYKNY Db 1708PPLPFA	QY 1253 GEMTQVRRRFERAIGPSQTH1	Db 1726	1313 ISLPNIRKPD	Db 1734 ISLPEISLPN 1743	SULT 10 S64673	AAS64673 PRELIMINARY; AAS64673;	DT 01-APR-2004 (IIEMBLEEL 27, Cre DT 01-APR-2004 (TrEMBLEEL 27, Las DT 01-APR-2004 (TrEMBLEEL 27, Las	CG33300-PA (Fragment). CG33300. Drosophila melanogaster (Fruit		OC Ephydroidea; Drosophilidae; Dro OX NCBI TaxID=7227;	RP SEQUENCE FROM N.A. RX MEDILIBE=20196006; PubMed=10731.	Andmis m.D., Cellitker S.E., Holling R.A. Amanatides P.G., Scherer S.E., RA. George R.A., I.ewis S. R. Brichs.	RA Sutton G.G., Worthan J.R., Yanda R.A. Brandon R.C., Kogers Y.H., Blac R. Wan K H DAVIE C DAVIE C DAVIE C	RA Abril J.F., Agbayani A., An H.J RA Ballew R.M., Basu A., Baxendale	
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E., Li P.W., Hoskins R.A., Galle R.F.,
Chards S., Ashburner M., Henderson S.N.,
Yandell M.D., Zhang Q., Chen L.X.,
Blazzel R.G., Champe M., Pfeiffer B.D.,
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H.J., Andrews-Pfannkoch C., Baldwin D.,
dale J., Bayraktaroglu L., Beasley E.M.,
rman B.P., Bhandari D., Bolshakov S.,
ouck J., Brokstein P., Brottier P., -----TTPETTTAAPt fly).

a; Hexapoda; Insecta; Pterygota;
era; Brachycera; Muscomorpha;
rosophila. VEVNPKSEDAGGAEGETP---reated) ast sequence update) ast annotation update) PLPEI----------TKAPKKPT----PRT; 1761 AA.

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra de Pablos B., Delcher A., Deng Z., Mays A.D., Dew. I., Dietz S.M., Ba Dodeon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Duzbin K.J., Evangelista C.C., Perraz C., Ferriera S., Fleischmann W., Ra Fobler C. Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Houston K.A., Howland T.J., Hernandez J.R., Houck J., Harris M., Harris N.L., Harrey D., Heiman T.J., Hernandez J.R., Houck J., Ra Houston K.A., Howland T.J., Wei M.H., Ibegwam C., Kalush F., Karpen G.H., Ke Z., Kennison J.R., Ketchum K.A., Ra Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Ra Lasko P., Lei Y., Mcrapen G.H., Ke Z., Kennison J., Moshrets D., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Rakulov G., Milshina N.V., Mozary C., Morris J., Moshrefi A., Ra Mount S.M., Moy M., Muxphy E., Muxphy L., Marzy D.D., Nelson D.L., RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H., Ra Svirskas R., Tector C., Turner R.D., Scheeler F., Shen H., Ra Svirskas R., Tector C., Turner R.D., Scheeler F., Shih T., Spier E., Spradling A.C., Stapleton M., Strong A.H., Wasserbach J., Wasserbach G., Wasserbach G., Wasserbach G., Wasserbach G., Turner R., Venter E., Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Ra Arbeng K.H., Zavori J.S., Zhong M., Zhuo S., Zhu X., Smith H.O., R. Arbeng X.H., Myers E.W., Rubin G.M., Venter J.C.;
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197521 MW; 62A5E16E6241B3F4 CRC64;

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973 KTSTTKTTRE--PTTKRKTTERTTKEPTTRKTTTHKTTEEPTTNKTTTKKTTHEPTTKKS 1030 855 595 915 670 799 571 628 91; 434 ---PITPKEPA-----PIAPKKPAPITPKEPAPITIFKEPAPITIKEPSPT-----TPK 479 520 739 445 348 391 563 621 47 AQCKKYDKCCPDYESFCAEVHNPISPPSSKKAPPPSGASQTIKSTIKRSPKPPNKKKTKK 106 -----TKKSTTLRTTEEPTTRKSST 191 нкттвврттккттнврттккзттькртввртткктзттктврттккттвкттвкттк 800 RKITTHKTTEEPTINK----TTTKKTTHEPTTKKSTTLKPTEEPTTRKTSTTKTTREPTT ------PITPKKPAPITPKEPA---------KAAAPNTPKEPAPTTPKEPAPTTPKEPA------PTTPKETA-----PTTPKG TA-----PITLKEPAPITPKKPAPKELA-----PITIKEPISITSDKPA-----P 622 THEPTTQKSTTLRITEEPTTRKSSTARTTRE--PTTKRETTERTTQEPSTSKTTTHETTA 856 KRETTERTTQEPSTSKTTTHETTAEPATKKTTHEPTTQKSTTLRITEEPTTRKSSTAKTT 916 RB----PTIKRETIERTIKEPITRKITITHKITEEPIIKKITHEPITKKSITLKPIEEPIIR KVLAKPTPKAET----TTKGPALTTPKEPTTTPKEPAS-TTPKEPT------PT 446 TRKSSTARITREPITKRETIERTIOEPSTSKIKHHETTAEPAIKKTTHEPITOKSTILRI KSTTLRITEBPTTRKSSTARTTRE--PTTKRETTERTTQEPSTSKTTTHETTAEPATKKT --RETTERTTKEPST SKTTTHE-----TTAEPATKKTTHEPT--TOKSTTLTEEPTRKSSTARTTREPT 244 ---ETKETTT-----TINKOTSIDGKEKITSAKETQ-----SIEKTSAKDLAPTS 388 KTTREPTTKRETTERTTKEP--STSKTTTHETAAEPATKKTTHEPTTOKSTTLRITEEPT ---PITPKEPAPITIKEPAPITIPKEPAPITIKEP------APITIKSA---PITP KEPA-----PITPKKPAPITPKEPAPITPKEPTTPKEPA------PITKEPA----BPAPTTTKSAPTTTKEPA-----PTTTKSA-----PTTPKEPSPTTTKEPA----**EPATKKTTHEPTTQKSTTLRITEEPTTRKSSTAKTTREPTTKRETTERTTKEPTTRKTTT** SKNSAANRELOKKLKVKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTT-----PDT ---SSSSSTIWKI Length 1761; 881; S-TIQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTV---------PTTPKEPAPTTTKKPA--PTAPK------EPA---Query Match
18.6%; Score 1349.9; DD 2; Deusymet Local Similarity 25.2%; Pred. No. 3.38-19;
Matches 472; Conservative 117; Mismatches 400; Indels PTTPKKLT--------EPA-DB 2; 18.6%; Score 1349.9; 25.2%; Pred. No. 3.3e ---KTTREPTTK--107 VIESEEITEEHSVSE--NQESSSSSSS---LANHLS------596 PEKPAPITPEELAPTIPEEPT-TIKSA-----PITPKE---|:| | RKSSTA----161 AETKK----572 PKETA---629 329 740 349 392 564 435 480 680 521 545 144 252 198 280 ð g g à g δ g à ð 음 d ð g ò qq ò g à qq à g ਨੇ à g ð 용 δ ð a ð

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                                                                                                                                                                              Length 251;
SEQUENCE FROM N.A.
Jones A.R., Hughes C.E., Flannery C.R., Caterson B.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY653038; AAT74746.1; -.
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GO; GO: 000812; P: receptor activity; IEA.
GO; F: receptor activity; IEA.
FEAM; PF04680; OGF_III; 80.
FEAM; PF04680; OGF_III; 80.
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0; Mismatches 4;
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119 PTSPP-----SSKKAPPPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEEHSV---Anopheles gambiae str. PEST. Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles. NCBI_TaxID=180454; Query Match 18.2%; Score 1324.3; DB 2; Length 3150; Best Local Similarity 17.9%; Pred. No. 3.4e-18; Matches 460; Conservative 135; Mismatches 481; Indels 1487; which 3150 AA; 322879 MW; 3C7B3D441CE8C839 CRC64; Anopheles Genome Sequencing Consortium; Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases. -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry w preliminary data. EMBL; AAABO10089800; EAA13969.2; -. 임

> Q6DNC4; Q6DNC4

RESULT 11

622	645 KEPAPTIPKEPAPTIPKETAPITEKGTAPTI 675	676 LKEPAPTYPKKPAPKELAPTTTKEPTST 703	TTMSSASTPEPSTTPG	725APTTP KEPAPTTPKGTAPTTLKEPAP 750 	751 762 : : : 2188 GTTRTTPTRPTSTRSSSMSSASTPE 2247	763 PITTKGPISTTSDKPAPTTPKETAPTTPKEPAP 795 - - - - -				. [⊢	832PDESTPELSAEP		2548 TIMSSASTPEPSTTPGTTRTTPTRPTPTDTTMSSASTPEPSTTPGTTRTTPTRPTSTDTT 2607	MSSSMSSASTPEPSTTRTTPTRPTPTDSTMSSSMSSASATPGTTRTTPTRPTSTES	900 TATTTEKTTESKITATTTQVTSTTTQDTTPFKITTLAP 942		TTPTRP	973 981 973 SKATTPKPO 981 978 SKATPKPTPTRPTRPTRPTBSSNSSASTPRPSTR 2847		: TRPTPTDSTMSSSMSSASTPEGTT	1001 RVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQ 1033	ALIETE TELEGISTICO DE LE LOCATION DE LA CONTROL DE LA CONT
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PARRIT		SSE	RP SEQUENCE FROM N.A. RA Ferris P. J., Waffenschmidt S., Umen J.G., Ishida K., Kubo T., Lau J., RA Goodencugh U.W.; R. Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases. B. Sharis AAS07044.1; DR EMBL; AAS07044.1; DR InterPro; IPR002951; Atrophin. DR InterPro; IPR003882; Pissil_extensin. DR PRINTS; PR01222; ATROPHIN. DR PRINTS; PR01218; PSTLEXTENSIN. SQ SEQUENCE 3409 AA; 336045 MW; 7FEB7633EDD6631F CRC64; GUETY MATCH OUETY MATCH AT. 08; Score 1237.4; DB 2; Length 3409; Best Local Similarity 14.0%; Pred; NO. 2.5e-16; MAtches 396; Conservative 166; Mismatches 471; Indels 1766.	VNVSVTSSAATDAPSAIAYIGALIDVLANVPWQPNCINDTRRSYD VVVSVTSSAATDAPSAIAYIGALIDVLANVPWQPNCINDTRRSYD VYDETYIDATVYSGNSLRPFYSTCRYPASSDPYAFLEPYSMPWVD FVIQOVSSQELSCKGRCFE 3 WGPTVNTVDSNLKWIDPAWTAQGAWLGGQDFRDAVWNFGTHYCSW 2 KYD

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QΩ	: 1761 TAATYPAVAATTTLVAAASSSFAQAIRAKGSLLQGSYHIQMLTMSLYLASRGV 1813	02-MAR-2004 (TrEMBLrel. 27, Plus agglutinin.	otatio
λΌ		SAG1.	orothers. Chloron
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δδ	PEETAKPKDRATNSKATTPKPQKP		
qq	SNTTASGSSSGSSSSNSP-PRRPPPPRAGSTGLLKSNADAS-FFLAVALFALFES		Umen J.G.
රු ස්	LMQQMLQPPAAAV	RT "Plus and Minus Sexual Aggluti RL Submitted (OCT-2003) to the EW	Sexual Agglutinins from Chlamy (003) to the EMBL/GenBank/DDBJ
3 8	PTSRIABAMLOTTTRPNOTPNSKLV	EMBL; AY450930; AAS07044.1; SEQUENCE 3409 AA; 336045	 MW; 7FE87633EDD66
7 음	AAPP	Query Match 17.0%;	Score 1237.4; DB Pred. No. 2.5e-16
ò	1049VNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINP 1096	vative 1	66; Mismatches 47
qu	2038 GRLIAAVLYRLLVSPE		YLLL
Qy	1097 MLSDETNICNGKPVDGLTTLRNGTLVAFRGH	50	VTSSAATDAPSA1AY1GA
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ζŎ	1128YPWMLSPFSPPSPARRITEVWGIPSPIDTVFTRCN 1162	Db 110 APWPSRCALPAVQYGYYDBTYIDATVYSGNSLRPFYS	ryidatvysgnslrpfys
ОС	2108 YAAFLWWLALARAWNVPQPTLVEPMTTSSYASPRPSAFERADRTSPRPST 2157	Qy 1.7FV	FVIQQVSSQELSCR
ζŏ	1163WR-FT 1179		VNTVDSNLKWIDPAWTAC
qu	2158 VSIATAADIGGTATGGGGGAASGACADVGAMAAPATVAAĞADVPSEDDRYARGPHWKQF- 2216	36 SFERGRECDC	DAQCKKYD
0y	1180 NDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVYFFKRGGSIQQYIYKGEPVQK 1239	230 PFVEC	ADPYDPDKIANGIVPAVI
qu	2217DGVLPPTVASGVGSGGGVVPL	54	
ζ	1240 CPGRRPALNYP	Db 284 SLDNVMYLNLAYNFIGGFLPANLFTLLFSLCHLALLF	РАМЬРТыьРЗЬОЯНАВЫ

-----pNIRKP----- 1322 ----RIARAI----- 1347 |: ||: |SGADVRSRRALNAEAVAAAAAGGG 2550 : | | | DHCRATPDVRGTASLQYGWQQYPST 343 PRGAAAGE-----DIH 2287 DGAATAGVGVDAAAGGAGGGGRG 2324 NAMSSGAASFGASAGGGGAAAASR 2384 SRAGSPPEGAGGYAGGANAMFAGT 2444 :|:| MTAGAVGVGGGVRRPAGSLRNASD 2504 GALLDVLWNVPWQPNCINDTRRSYD 109 YSTCRYPASSDPYAFLEPYSMPWVD 169 VITALDFRNASLYIYYLDFGMFPAG 283 :| AQGAWLGGQDFRDAVWNFGTHYCSW 229 ---KCCPD----- 58 LLLLSV----- 16 CKGR----CFE 35 DB 2; Length 3409; 16; 471; Indels 1796; Gaps nida K., Kubo T., Lau J., mydomonas reinhardtii."; J databases. ophyceae; Volvocales; 6631F CRC64; date) update)

	1461 LVGGSSRGNNTNGSSSGGNYYSNGGDAAIQRIPAGNSTDRGGSSSGSGGSSSWGPGTETA 1520 875KDKTTERDL	1641 TAAGSSSSGTSRSGNGNGTAAAAAAPPPPAGTTGRRRALQQQAAPPPPASGSSSSL 1700 914ATTTQV 919 1701 SGAATANQQQRHVHFLLPATAYADAARNPGRNDLSLSVELTDNAVASPAVGEALATTRV 1760 920 TSTTQDTTPFKITTLTAPKVT	946INNK 959 1814 GREYGEYAVEFKYAVLGVKGNLGPAEAAMPTNEKEVTAAEQARQVGGDLWFIGNDLLGGS 1873 960 PEETAKPKDRATNSKATTPKPQKP		1057 MEADEINICHGEAUNGLITIANGTILVALTEYSCMALGGDAADWHGSRTAAYCULTIAVUP 2107 1128TTIAGLILVALTEYSCMALGGDAADWHGSRTAAYCULTIAVUP 2107 1128YFWMLSPFSPPSPARRITEVWGIPSPIDTVFTRCN1162 2108 YAAFLWWLALARAWWVPQFTLVEPWTTSSYASPRPSAFERADRTSPRST 2157 1163
PDEWGDAVAAASDSSLPWANLRTVRLSNQALYGSFCAEVHN					10.49 PRSPEPSPAPTTPEEPAPTTPKAAPNTPKEPAPTTPKEPAPTTPK 653

-S-D-E- Gaps	A KTLPIYLLLLSVFV	143 58
Db 2244 LPGSGRHLPLPPLLPAAGAATAAGGGAATAPGSPRGAAGE		REBURY 155 AC Q06852. AC Q06852. AC G1 Surface elyoprotein 1 precursor (Outer layer protein B) (S-layer Colstridian thermocellum. AC G1 Surface elyoprotein 1 precursor (Outer layer protein B) (S-layer Colstridian thermocellum. AC G1 Surface elyoprotein 1 precursor (Outer layer protein B) (S-layer Colstridian thermocellum. AC G1 Surface elyoprotein 1 precursor (Outer layer protein B) (S-layer Colstridian thermocellum gene cluster encoding the C1 Colstridian. AC G1 Surface Elox N. A. Mueer JP. AC G1 Surface Elox N. A. Mueer J. A.

	414TPK-EPTPT-TPXEPAPT-TKEPAPTTPKEPAPTAPKKPAPTTPKEPAPT- 460	52	56		622 EPAPITPKAAAPNTPKEPAPITPKE	n o	1113 PTPSDEPTPSD-EPTPSDEPTPSETPEEPIPTDTPSDEPTPSDEPTPSDEPTPS 1165 738 KGTAPTTLKEPAPT-TPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEP 793	EPTPSD-EPTPSDEP 12	794 APT-TEKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSP 852	853 KEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKI	1267 EEP-IPTDIPSDEPIRSDEPIRSDEPIPSDEPIPSDEPIPSDEPIPSDEPIPSEPIPSEPIP	1326 PIDTPSDEPTPSDEPTPSDEPTPSDEPTP 1360	STKKPKTMPRVRKPKTTPTPRMTS	1361 SDEPTPSDEPTPSETPEEPTPTTTPTPTPTPTSGSGGSGGGGG 1407	1017TMPELNPTSRIABEAMLQTTRPNQTPNSKLVBVNPKSEDAGGAEGETPHMLL 1068 1408 GGGGTVPTSPTPTPTSKPTSPPAPTRIR-BPTDSNVDGATGGEDAAVT 1466	RVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHY 112	1456 RSFR 1464	FWMLSPFSPPSPARRITEVWGIPSPIDTVFTRC	PERNIT		DLADTHWAAWAI	KC		30	1301 LWRGLPNVVISAISLPNIRKPDGYDYYAFSKDQYYNID 1338
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1620 -INGAPKL-----FPDVNE----SYWAFGDIMDGALDHSYIIE 1652 Dp

Search completed: October 13, 2004, 12:19:10 Job time : 188.862 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

OM protein - protein search, using sw model

Run on:

October 13, 2004, 11:23:49; Search time 27.7629 Seconds (without alignments) 4723.689 Million cell updates/sec

Perfect score:

1 MAWKTLPIYLLLLLSVFVIQ.....ARAITTRSGQTLSKVWYNCP 1363 Sequence:

Scoring table:

0.1 BLOSUM62 Gapop 10.0 , Gapext

Total number of hits satisfying chosen parameters: 283416 seqs, 96216763 residues

283416

seq length: 0 seq length: 200000000 B B Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C;Species: Homo sapiens (man)
C;Date: 10-Mar-1993 #sequence revision 12-Apr-1996 #text_change 09-Jul-2004
C;Date: 10-Mar-1993 #sequence revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: A49963; A45106; B4106; A43932; B31532; A61257; P00328; P00329
R;Gum Jr., Jr.R.; Hicks, J.W.; Toribara, N.W.; Siddiki, B.; Kim, Y.S.
J. Biol. Chem. 269, 2440-2446, 1994
A;Title: Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of the A;Reference number. A49963; MUID:94132002; PMID:8300571

A Molecule type: mRNA
A; Residues: 1-639 <GUI>
A; Residues: 1-639 <GUI>
A; Cross-references: UNIPROT: Q02817; UNIPROT: Q14884; GB: L21998
A; Cross-references: UNIPROT: A: Toribara, N.W.; Rothe, E.W.; Lagace, R.E.; Kim, Y.S.
J. Biol. Chem. 267, 21375-21383, 1992
A; Title: The human MUC2 intestinal mucin has cysteine-rich subdomains located both upst: A; Reference number: A45106; MUID: 93016075; PMID: 1400449 A, Accession: A45106 A, Status: not compared with conceptual translation

A Molecule type: mRNA A;Residues: 626-1895 <GU2> A;Residues: 626-1895 <GU2> A;Cross-references: GB:M94131; NID:g186395; PIDN:AAAS9163.1; PID:g186396 A;Note: sequence extracted from NCBI backbone (NCBIP:116706) A;Accession: B45106 A;Status: not compared with conceptual translation

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A;Rosidues: 2037-3020 <GU3>
A;Nolecule type: mRNA
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A;Rosidues: 2037-3020 <GU3>
A;Rosidues: 2037-3020 <GU3>
A;Rosidues: GB:MA9132; NID:g186397; PIDN:AAA59164.1; PID:g186398
A;Rxperimental source: colon
A;Note: sequence extracted from NCBI backbone (NCBIP:116698)
R;Toribara, N. W.; Gum Jr., J.R.; Cilhane, P.J.; Lagace, R.E.; Hicks, J.W.; Petersen, G.N.
J. Clin. Invest. 88, 1005-1013, 1991
A;Title: MUC-2 human small intestinal mucin gene structure. Repeated arrays and polymorf
A;Reference number: A43932; MUID:91358717; PMID:1885763
A;Nolecule type: DNA
A;Residues: 1343-1350, L',1352-1411, S',1413-1448, P',1450-1503, T',1505-1915 <TOR>
A;Note: sequence stracted from NCBI backbone (NCBIN:55749, NCBIP:55750)
A;Note: sequence thromaistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:55749, NCBIP:55750)
B;Gum, J.R.; Byrd, J.C.; Hicks, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.S.
J. Biol. Chem. 264, 6480-6487, 1989
A;Ritle: Molecular cloning of human intestinal mucin cDNAs. Sequence analysis and eviden A;Reference number: A33532; MUID:89197956; PMID:2703501

A, Molecule type: mRNA A, Residues: 1916-2193 <GU4>

A,Cross-references: GB:W12405; NID:g188873; PIDN:AAA36334.1; PID:g188874 A;Experimental source: intestine R;Jany, B.H.; Gallup, M.W.; Yan, P.S.; Gum, J.R.; Kim, Y.S.; Basbaum, C.B.

Db 1210 SCVCTNSSQVVCRPEEGKILNQTQDGAFCYWEIGGPNGTVEKHFNICSITTRPSTLTTFT 1269 Qy 242TVETKETTTTNKOTSTDGKEKTTSAK	334 1450 392 1508 144 1568 504	1680 TPSSPITTTPSPPTTPITTPSSPITTTTPSSTTTP-SPPTTMTT 623 PAPTTPKAAAPNTPKEPA	
J. Clin. Invest. 87, 77-82, 1991 A, Title: Human bronchus and intestine express the same mucin gene. A, Reference number: A61257; MUID:91086481; PMID:1985113 A, Accession: A61257 A, Status: not compared with conceptual translation A, Molecule type: mRNA A, Residues: "Y, 1252-1944, TTS', 1952-1954 <jan> A, Residues: "Y, 1252-1948, TTS', 1952-1954 <jan> A, Experimental source: bronchus R; Xu, G.; Huan, L.; Khatri, I.; Sajjan, U.S.; McCool, D.; Wang, D.; Jones, C.; Forstner, Biochem: Biochem: Biochys. Res. Commun. 183, 821-828, 1992 A, Fitle: Human intestinal mucin-like protein (MLP) is homologous with rat MLP in the C-t A, Reference number: PQ0328; MUID:92198477; PMID:1550588 A, Molecule type: mRNA A, Molecule type: mRNA</jan></jan>	AyResidues: 2328-2468 < XUG> AyResidues: 2328-2468 < XUG> AyResidues: 2328-2468 < XUG> AyResidues: 2328-2468 < XUG> AyAccession: PQ0229 AyAccession: PQ0229 AyAccession: PQ0229 AyAccession: PQ0229 AyGenetics: AyGene: GDB:NUC2 AyGene: GDB:Nuc2 Ay	3 WKTLPIYLLLLLSVFVIQQVSSQELA 649 WREHVCNKDVGSCPNSQVFLYNLTTCQCTCRSLSI 39 RGRECDCDAQCKKYDKC-CI (1) RGRCVPLAKCSCYHRGLYLEAGDVVNQEERCVCI 68 NPTSPPSGKAPPPSGASQTIKS 769 SNLTALATSKPRALSCYLLAAGXYHTECVSG 101 KKKTKKVIBSEITEEHSVSENQESSSSSSSSSSS 101 KKKTKKVIBSEITEEHSVSENQESSSSSSSSSSSS 150	4 7 7

A.Reference number: Z18847; MUID:93209931; PMID:8458832
A;Accession: T18262
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1664 <FUJ>A;Residues: 1-1664 <FUJ>A;Cross-references: UNIPROT:Q06852; EMBL:X67506; NID:g296879; PID:g296881; PIDN:CAA47841 cluster encoding the cellulosom RESULT 2
T18862
5.1ayer protein - Clostridium thermocellum
C,Species: Clostridium thermocellum
C,Species: Clostridium thermocellum
C,Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C,Accession: T1826
C,Accession, T1; Beguin, P.; Aubert, J.P.
F,Fulino, T.; Beguin, P.; Aubert, J.P.
J. Bacteriol: 175, 1891-1899, 1993
A;Title: Organization of a Clostridium thermocellum gene cluster encoding t)

DB 2; Length 1664;

16.4%; Score 1190.4;

265 FAGYQLNIKYDPIMLEAIELETGSAIAKRTWPVTGGTV----LQSDNYGKTTAVAND 486 298 AGIINFAEAYSNLTKYRETGVÄEFTGIİGKIGFRVLKAGSTAİ-----RFEDTTAMPG 541 661 359 176 721 460 TPKEPAPITIKEPSPITIKEPAPITIKSAPITIKEPAPITIKSAPITPKEPSPITIKEPA 520 PITPKEPAPTITPKKPA-------PITPKEPAPI-TPKEPAPITIKKPAPTAPK 565 -----ETSLTVNKETTTVETKETTTTNKQTSTDGKEKTTS----YVIMELDKTKVKEGDVIIATIRVNNIKNLAGYQIGIKYDPKVLEAFNIETGDPIDEGT PAVGGTILKNRDYLPTGVAINNVSKGILNFAAYYVYFDDYREEGKSEDTGIIGNIGFRV 360 TKEPAPTTPKEPA----PITTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKKEPAPT-------AKETQSIEKTSAKDLAPTSKVLAKPTPKAETTT--------EPAPTTTKSAPTTPKEPAPTT 722 LKAEDTTIRFEELESMPGSIDGTYMLDWYLNRISGYVVIQPAPIKAAS-----DEPIPTD -----TPK-EPTPT-TPKEPAPT-TKEPAPTTPKEPAPTAPKKPA--PTTPKEPAPT-330 IKSAPTTPK-----414 461 897 521

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                                                                                          TATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTBIMNKPEETAKPKDRATN
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                                         EPAPTTPKAAAPNTPKEPAPTTPKEPA--PTTPKEPAPT-TPKETAPTTPKGTAPTTLKE
                                                                                                                             PAPTTPKKPAPKELAPTTKEPT-STTSDKPAPTTPKGTAPTTPKEPAPTTP
                                                                                                                                              KGTAPTTLKEPAPT-TPKKPAPKELAPTTTKGPTSTTSDKPAPT---TPKETAPTTPKEP
                                                                                                                                                                                                                                794 APT-TPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSP
                                                                                                                                                                                                                                                                                 KEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKI
                            EPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPT---TPEELAPTTPEEPTPT-TPE
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                                                                   Nillernate names: alpha-NAC protein
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30826
R;Yotov, W.V; St-Arnaud, R.
Genes Dev. 10, 1763-1772, 1996
A;Title: Differential splicing-in of a proline-rich exon converts alphaNAC into a muscle
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920 336 979

--PKEPTPTTIKSAPTT

305

--TPKAETTTKGPALTT----

207

---NKVST

687

SPEIPKSV------PFPDPPLAEISFSNARKVDAVSHMESSGSSRQGHPDASV

247

802 283 860

-----KDLAPT

SPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKE

TTTTNKQTSTDGKEKTTSAKETQSIEKTSA---

TAKGTVVCLADSSLDTSVSASKGSALSGASSPLYPLEVSFLPEAGLAVQGPKGSLNKLSP 747

TQH-----

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688 208 748 248

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A,Reference number: 220889; MUID:96312450; PMID:8698236
A,Accession: T30826
A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residuse: 1-2187 <YOT>
A;Cross-references: UNIPROT:P70670; EMBL:U48363; NID:g1666688; PID:g1666689; PIDN:AAB187
A;Cross-references: A;Genetics:
A;Genetics:
A;Genetics:
A;Amap position: 1
B;Molecule tyl; 1996/1; 2024/3; 2050/3; 2099/3; 2142/3; 2183/3
A;Mutroms: 24/1; 1996/1; 2024/3; 2050/3; 2099/3; 2142/3; 2183/3
A;Mutroms: 24/1; 1996/1; Bylicing converts alphaNAC into a tissue-specific DNA-binding active C;Keywords: alternative splicing; DNA binding; transcription factor 86; 460 199 126 520 140 580 151 640 282 400 122 342 80 80 581 VSQPLKRSVTDPAMAPRTAKNTAPSTTSPLVPLASEGCPVASSMALSPQNASVSETALAL 183 QVPSQGTLNLKGTA------PCPPDVVRAFPSHLENPLASVQPGLM 283 LIHISSVDSPIQPPGQSGLAVSNPTSVGHSGIAASCPPERCVVPALPSRLLAVDSGAAPSD PVSCIGATHHALDNPSAISVAPATHVPPPTSSGLVSSKDPASPVTSLVVPAAHKQFPAPP 461 ASATLGVPVSPLPATEGLKNLPISALVNVGAPVSPAQAGLPTRKDTTLQPLAPIALKESP VDEAGSGLDNGDFKVTTPDTST 223 SCPQTLSNTSPVKGVPISSALTQSRLSLNLKGPVSPPARNTAAPSIPLAPSTSLGCHLPL SSOSASSLEVLSEDTVTKKTTGGPAPVVRPAIAGVATTTSLRADSPPAVIRADSCVSPNT Query Match

14.6%; Score 1065.3; DB 2; Length 2187;
Best Local Similarity 18.6%; Pred. No. 1.7e-14;
Matches 413; Conservative 171; Mismatches 486; Indels 1147; QVSSQ-ELSCKGRCFESFERGRECDCDAQCKKYDKCCPD-YESFCAEVHNP------TSPPSSKKAPP --ELOKKLKVKDNKKNRTKKKRPTPKPPV----PSGASQTIKSTTKRSPK --IKSSKNSAANR---SSSSSS----SSSTIMK---ESEEITEEHSVSEN-----521 152 109 401 127 343 123 141 21 70 81 81 g g g ð q à ò à g à a ò Db ò à à g

	Query Match 14.64; Score 1061.4; DB 2; Length 7962; Best Local Similarity 15.34; Pred. No. 3.3e-13; Matches 429; Conservative 152; Mismatches 508; Indels 1716; Gaps 106; QY
C C C C C C C C C C C C C C C C C C C	14 TIERPAPTTPKKPAPPELAPTTIKCPTSTISDKPAPTTPKETAPTTPKRAPA 803 15:

seq1-f.rpr

	236TUNKETIVETKETTTINKQTSTDGKEKITSAKETQSIEKISAKDLAPISKUJ. 287 679 IMSTAIPSSTBETUHTSTULTTATTGATGSVALP8STPGTAHITKULT 728 288AKP	
6 6 6 6 6 6	8 6 8 6 8 6 8 6 8 6	6 R 6 R 6 R 6 R 6 R 6 R 6 R 6 R 6 R 6 R
QY 1235 EPVQKCPGRRPALNYPVYGEMTQVRRRRFERAIGPSQTHTIRIQYSPA 1282 Db 7848 SP	RESULT 5 T45025 mucin MUC5B, tracheobronchial [imported] - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 21-40a-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000 C;Accession: T45025 R;Desseyn, J.L.; Guyonnet-Duperat, V.; Porchet, N.; Aubert, J.P.; Laine, A. J. Biol. Chem. 272, 3168-3178, 1997 A;Title: Human mucin gene MUC5B, the 10.7 kb large central exon encodes various alternat A;Reference number: Z22899; MUID:97166151; PMID:9013550 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecule typ	Query Match 14.5%; Score 1052; DB 2; Length 3570;

	2640 TVRTAWTSATSGTLGTTHITEPSTGTSHTPAATTGTTTTSTPALSSPHPSSRITTESPPSP 872TTAKDKTTE	928 -TPFKITTLKTTTLAPKYTTTK KTITTTEIMNKEBETAKEKDRATUSKATTTAKEKDRATUSKATTTAKEKDRATUSKATTTAKEKDRATUSKATT	DD 3120 ATALPALKSTATTPTATESSLGTTWTRLSQTTTPTATMSTATP\$STPETVHTST 3179 QY 1027 IAEAMLQTTTRPNQTPNSKLVEVNPKSEDAG-GAEGETPHMLLRPHVFM 1074 : :	1138	RESULT 6 T16251 Typothetical protein F35A5.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004 C;Accession: T16251
		TATALPALES OF THE SSSECTION OF THE SSSEC	HGRS 2103 T 751 SSRT 2163 KEP- 793 CEPQ 2219	CAWSEWLDYSYPMPGPSGGDFDTYSNIRAAGGAVCEQPLGLECRAQAOFGVPLRELGQVV 2279	

⁰⁹⁻Jul-2004

R;Leimbach, D. submitted to the EMBL Data Library, January 1996 A;Description: The sequence of C. elegans cosmid F35A5. A;Reference number: 218485 A;Reference number: 218485 A;Recession: T16251 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-1274 <lei>A;Residues: 1-1274 <lei>A;Residues: 1-1274 <lei>A;Resperimental source: strain Bristol N2; clone F35A5 A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Aintrons: 1272/2</lei></lei></lei>	Db 641 EPISKPKDTAPKKAEPNSPVVP-PTEVKNKPPWEDDDAPAKPVSLPEPEKKTP 697 Qy 661KETAPTTPKGTAPTTLKEPAPTTPKKBAPK-ELAPTT 696
DB 2; Length 1274; 14; 30; Indels 748; Gaps 8	
ref	: :
OT 25 71 LT 30	OY 886 TPETITAAPKMIKETAITITEKITAESKITAITIQU 926
305 TPKEPTPTTPKEPASTTPKEPTPT	
371 229 420 283	QY 1073 FMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWML 1132 Db 1219PTEPPKPAAPKKWED 1237 QY 1133 SPFSPPSPARRITEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDIKDAG 1186 Db 1238 DPDEPEADFTWPAPKKPDTEDPADSL
4 4 8 8 3 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	Qy 1187 YPKP 1190 Db 1265 GPKP 1268
	AESULT 7 T31108 Cyst germination specific acidic repeat protein precursor - Phytophthora infestans Cyst germination specific acidic repeat protein precursor - Phytophthora infestans C;Species: Phytophthora infestans (potato late blight agent) C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004 C;Accession: T31108 R;Goernhardt, B. R;Goernhardt, B. A;Meference number: Z2098
582 615 640 660	A;Accession: T31108 A;Accession: T31108 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1489 <ggc> A;Cross-references: UNIPROT:096449; EMBL:AF061185; NID:g3851513; PID:g3851514; PIDN:AAC7 C;Genetics: A;Gene: car90 Query Match 14.0%; Score 1020.2; DB 2; Length 1489;</ggc>

7		
ï		Db 1094
g G	IPCSGVGAEPVGIACFRAGDVAISDCQPIDDSINGAVCVAEVDABCADIRDDRAGGE	δλ
δλ		Db 1154
Op Op	101 PKTGYTSAVEAETIAAYNGESSGWGTGHDEVVQVGDEEEEIPARVNYDTTVDTPIGVNCE 160	λŏ
δy	79	Db 1212
Db	161 VATETATQGHATEGGKXYDTPSTGTQTGDYGNTIHYGSTTTEGVTKGGYGPTDAKV 216	ò
δλ	108 IESE 111	Db 1251
qq	1: 1 217 IDGETYLDYPTGITEIIEDGTTPGGYGTTTDGGTTTGGYTTVDNTHETTBGAGGYDAGTR 276	
ζ	112EITEEHSVSENQESSSSSSSSSSTIWKIKSSRNSAANRE 152	Db 1309
q _Q	277 EEYSTTPTVGXSTEETEGQHVTGGXEPSDETEAPTEGTTYVPREETTAAPSEDTTYAPRE 336	
ζ	153 LQKKLKVKDNKKNRTKKKPTPKPPVVDEAGSGLDNG	Db 1344
Db	337 VTPYAPTEKPYDVEETTYVTEESTYAPTKSETNAPTERMHYAHIEKP 383	Qy 1041
δλ	189 -DFKVTTPDTSTTQHNKVSTSP-KITTAKPINPRPSLPPNSDTSKETSLTVNKETT 242	1391
Db	43	Qy 1099
ο,	PKAETTTK 29	Db 1406
qo	439 YAPTEETTYAPTEKTTYAPTEETTYAPTEETPYEPTEETTYAPTKETTYAPTEETTY 495	Oy 1155
λ		Db 1429
qq	496 ASTEETTYAPTBETTYAPABETPYEPTEET-TYAPTEETTYAPTEETTYAPTTEETTYAPT 554	Qy 1208
δλ		Db 1465
Dp	555 EETTYAPAEETPYEPTEETTYAPTEETT-YAPTEETMYAPIEETTYAPTEETTYAPAEET 613	Qy 1262
δy		Db 1485
qq	614 PYEPTBETTYAPTEBTTYAPTBETTYASTBETTYÄPTEBTTYAPÄBETPYEPTETTYÄP 673	
δγ	444 TAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPT-TTKSAPT 491	RESULT 8 S48478
qq	674 TESTTYAPTESTTYAPTESTTYAPTESTTYAPASETPYEPTESTTYAPTESTTYAPTEST 733	glucan 1, ' N;Alterna
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Пb	734 MYAPIBETTYGPTEETTYAPITEATTYAPITEETPYAPITEETTYKEPTGETTYAPITEETTYAP	C, Accessic R, Rowley,
QY	530 TTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKBPAPTTPK 573	submitted A;Referen
QQ	794 TEETTYAPTEETTYAPTEETPYEPTEETTYAPTEETPYÉPTEETTYTPTEETTYÄPTEET 853	A; Accessic
ò	574 ETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPT 610	A; Residue
qq		R;Yamashi
δδ	611TPKEPAPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTT 651	A,Title: A,Referen
Dp	914 TEBTTYAPABETPYEPTBETTYAPTBETTYAPTBETTYAPTBETTYAPTBETTYAPTBET 973	A; Accessi
λõ		A; Residues: 1-2. A; Cross-reference
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PTKAPKKPTSTKKP-KTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQ 1040
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                                                                                                                                                                                                                                                                                                                                ETTYAPTEETTYAP-TEETMYAPIDETTYGPTEETTYAPTEATTYAPTEE 1308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------RNSQSWHSCCRSCYND------PICHAFSFHQTSSDSVCELT 1464
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EETTYAPTEETTYASTEETTYAPTEETTYAPAEETPYEPTEETTYAPTEETTYAPTEET 1093
                                                                                                                YAPTEETTYAPTEETTYAPAEETPYEPTEETTYAPTEETTYAPTEETMYAPIEETTYGP 1153
                                                                                                                                                                                                                           RDLRITPELTIAAPKWIKET----ATT---TEKTIBSKIJAITIQVISII----TOD 926
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                                                                                                                                                                             STISDKPAPITPKETAPI--IPKEPAPITPKKP----APPITPETPPPITSEVSTPI- 820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYBPTGETTYAPTEETTYAPTEETTYAPM------EET----
                                                                PAPTTPKGTAPT--TLKEPAPTTPKKP----APKE---LAPT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .PTDE------
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ha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae) mes: extracellular glucoamylase; mucin-like protein MUC1; protein YIR019c charomyces cerevisiae -1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004 48478; A26877; B26877; S27281; JC6123

he EMBL Data Library, October 1994 mber: S48478 48478

B: DNA

e: DNA 2-1331 «YA2» nces: EMBL:M16165; NID:g172523; PIDN:AAA35015.1; PID:g172526 e: DNA 242 «YAM» nces: EMBL:M16164; NID:g172522; PIDN:AAA35014.1; PID:g172525 26877

QY 579 TPKKLIPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPAPTTPKAAAPNTPKE 638	OY THE KITTATTT	RESULT 9 T29757 T20757 Crotein UNC-89 - Caenorhabditis elegans Cropecies: Caenorhabditis elegans Cropecies: Caenorhabditis elegans Cropecies: Caenorhabditis elegans Cropecies: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 03-Dec-1999 Crocession: T29757 R;Du, Z.; Le, T.T.; Wilson, R.
R;Pardo, J.M.; Ianez, E.; Zalacain, M.; Claros, M.G.; Jimenez, A. PEBS Lett. 239, 179-184, 1988 A;Title: Similar short elements in the 5' regions of the STAZ and SGA genes from Sacchar A;Reference number: S27281; MUD:89031230; PMID:3141213 A;Recession: S27281 A;Rolecule type: DNA A;Residues: 1-31 <par> A;Cross-references: EMBL:X13857; NID:94551; PIDN:CAA32069.1; PID:94552 B;Cons-references: EMBL:X13857; NID:94551; PIDN:CAA32069.1; PID:94552 R;Lambrechts, M.G.; Bauer, F.F.; Marmur, J.; Pretorius, I.S. B;Proc. Natl. Acad. Sci. U.S.A. 39. 8419-8424, 1996 A;Ritle: Mucl. a mucin-like protein that is regulated by Mss10, is critical for pseudohy A;Reference number: JC6123; MUD:96323237; PMID:8710886 A;Recession: JC6123 A;Recession: JC6123 A;Recession: JC6123; MUD:91304386; PIDN:AAC49609.1; PID:91304387 A;Residues: 1-1367 <lam> A;Residues: 1-1367 <lam> A;Residues: GB:U30626; NID:91304386; PIDN:AAC49609.1; PID:91304387 C;Genetics: A;Genetics: A;Genes: MPS:YIR019c; SGD:S0001458 A;Genes: SGD:MUC1; STAZ; MALS; DEXZ; SGD:S0001458 A;Genes: SGD:MUC1; STAZ; MALS; DEXZ; SGD:S0001458 A;Genes: SGD:MUC1; STAZ; MALS; DEXZ; SGD:S0001458 A;Genes: SGD:MUC1; STAZ; MALS; DEXZ; SGD:S0001458 A;Genes: SGD:MUC1; STAZ; MALS; DEXZ; SGD:S0001458 A;Genes: SGD:MUC1; STAZ; MALS; DEXZ; SGD:S0001458 A;Map position: 9R C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase C;Keywords: glycosidase; hydrolase; polysaccharide degradation; transmembrane #status predicted <tml. #status="" <tml.="" <tml.<="" domain:="" f;3-51="" f;5-21="" predicted="" td="" transmembrane=""><td>Query Match Best Local Best Local Matches 377 118 36 197 197 197 225 225 365 365 414 421</td><td> OY</td></tml.></lam></lam></par>	Query Match Best Local Best Local Matches 377 118 36 197 197 197 225 225 365 365 414 421	OY

QY 1098 GLTTLRNGT 1120 Db 3502 EVREQETLDLKVTVIGTPVPNVEWFKDDKPINIDNSHIFAKDEGSGHHTLT 3552 QY 1121 LVAFRGH	3613 1155 3673 1173	Db 3733 DQPVBIGQHWQLEVLEDGNIKLTIQNAKKEDVGAYRCEAVNVAGKANTNADLKIQFAAKV 3792		ALNYPVYGEMTQVRRRRFERA	4085 LVIEDSKTDDQGNYRIEVSNDAGVANSKVPLTVVESETLKIKKGLTDVNVTQGT 1309	QY 1313	OY 1323 1340 Db 4319 VPITVKQGETATENVKYKGPVKGVKWYKNGKEIPDAKTKDNGDGSYSLEIPNAQVEDAAD 4378 QY 1341SRTARAITTRSGQTLSKV 1358 Db 4379 YKVVVSNDAGDADSSAALTVKLADDGKDKVKPEIVSGLIPTTVKQGETATFNVKVKGPVK 4438	4439 QVKWY WY 4513 QVKWY 4513 Pothetical protein Species: Caenorhab
786 791	WYIGTQLVCATEDTEISNANGVYTMKI APTTPET I PVEFETSLCDATCREGDTLKLRAVLL TKEPTT	KATSE	VGDDLTEDESLREEMHRTPTPVMAPKFITKIKDTKAKKGHSAVFECVPOTTKCOCK	CEATL ETATT EKNPN	3040 SEKTITGENLIATIO	970	TAKASNPAGTAESSAEAEVTQSLEKPTFVRELVTTFVINET	1062 ETPHMLIRPHVFWIPEVTP
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C,Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004 C,Accession: T34513 R;Favello, A., Vaudin, M. submitted to the EMBL Data Library, August 1994 A,Description: The sequence of C. elegans cosmid ZK783. A,Reference number: Z21536 A,Accession: T34513 A,Status: preliminary; translated from GB/EMBL/DDBJ A,Status: preliminary; translated from GB/EMBL/DDBJ A,Residues: 1-3507 cRAv> A,Gross-references: UNIPROT:Q23587; EMBL:U13646, PIDN:AAC24418.1; GSPDB:GN00021; CESP:ZR A,Experimental source: strain Bristol N2; clone ZK783	Genetics: Gene: CSSP:ZK783.1 Gene: CSSP:ZK783.1 Inbrons: 14/1; 48/2; 84/1; 196/3; 303/1; 381/1; 586/1; 605/1; 1175/3; 1207/1; 1409/2; 504/1	Query Match 13.3%; Score 965.1; DB 2; Length 3507; Best Local Similarity 14.5%; Pred. No. 6.6e-12; Matches 453; Conservative 199; Mismatches 512; Indels 1959; Gaps 108;	19 IQQVSSQBLSCKGRCFESFE-RGRECDCDAQCKKYDKC 55 ::: : : : : : : : : :	56 59 	- BSFCABUH	626 VATRSNHSTSDQLITQVVQQSRNFSTGQLILTRGKVSSGBAVTQTTDADEFCLEISAADL 685 68NPISPPSSKAPPPSGASQTIKST 91 68		OBSESSESSES (DESCRIPTION OF THE PROPERTY OF T		147 159 923 ETTSRKPIEGSDSLFEGSGSGEMPETGSKGHFESGSKVSVTSGKGPTQSGAEGSGSGPKV 982	160 163	STATE OF THE TEXT OF THE TEX	DTSKE	233 TSLTVNKETTVETKETTTTINKOTSTDGKEKTTSAKET 269 	270 QSIEKTSAK DLAPTSKVLAKPTPKAETTTKGPALTTPKEPT 310 : : ::

©;Species: Rattus norvegicus (Norway rat)
C;Species: 13-May-1992 #sequence revision 13-May-1992 #text_change 09-Jul-2004
C;Accession: A42663; A41819; A31966; B20593; A20593
R;De Clercq, N.; Hemschoote, K.; Devos, A.; Peeters, B.; Heyns, W.; Rombauts, W.
J. Biol. Chem. 267, 9884-9894, 1992vos, A.; Poeters, B.; Heyns, W.; Rombauts A;Title: The 4.4-kilodalton proline-rich polypeptides of the rat ventral prostate are ti A/Status: not compared with conceptual translation
A/Status: not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-5762 < DEI>
A/Residues: 1-5762 < DEI>
A/Residues: 1-5762 < DEI>
B.; Hemschoote, K.; Peeters, B.; Dirckx, L.; Claessens, F.; De Clercq, N.; Heyns, W.; Wind
J. Biol. Chem. 263, 19159-19165, 1988
A/Title: A single 12.5-kilobase androgen-regulated mRNA encoding multiple proline-rich p
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A;Residues: 2020-2057 <PEE>
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A;Molecule type: protein
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A;Accession: A20593
A;Molecule type: protein
A;Residues: 2822-2859 <PEE>
A;Molecule type: protein
A;Residues: 2822-2859 <PEE>
A;Note: this peptide, designated proline-rich polypeptide IV, can be found at several loc C;Genetics:
A;Introns: #status absent the introns
C;Genetics: single copy gene with no introns
C;Superfamily: rat prostatic proline-rich peptides 637K precursor
C;Keywords: prostate; tandem repeat
F;1-26/Domain: signal sequence #status predicted <AGG>
F;27-5761/Product: prostatic proline-rich peptides 637K proprotein #status predicted <AAA A.Molecule type: mRNA
A.Molecule type: mRNA
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A.Molecule type: mRNA
A.Gross-references: 3372-3540 eHEM>
A.Gross-references: 3372-3540 eHEM>
A.Gross-references: 372-3540 eHEM>
A.Gross-references: 38.14206-14211, 1983
J. Biol. Chem. 258, 14206-14211, 1983
A.Title: Proline-rich polypeptides bound to rat prostatic binding protein. The primary A.Reference number: A94675; MUID:84061859; PMID:6685733 A;Experimental source: Ventral prostate.

A;Note: sequence inconsistent with the mucleotide translation

A;Note: sequence inconsistent with the mucleotide translation

B;De Clercq, N.; Hemschoote, X.; Devos, A.; Peeters, B.; Heyns, W.; Rombauts, W.

B;Reference number: A41819

A;Reference number: A41819 3277 --NQGKLSVYCEADGWTLVLGNETADFEGKIFVKGQAENPYCSKSFSSLLNSRKPYVFKV 3334 3335 VFQHCDVQLLDNHTMASTVVVQKHAMFLTNKADSYDLRCQYPIGSRAVESHVNVSELATT 3394 --RTARAITTR 1350 3395 STLTEKNSTLAPICRLSVSNDQHSSISSAMVGDTLKLALEVTPSENFGLLPRNCFAINIE 3454 150; Query Match
12.6%; Score 919.5; DB 2; Length 5762;
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 2792 HAEGQEESRAPPHFSLQPLDQEI	425	λō
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2732 GKIYLHYABPPTGPFVEPPDLF		δ
682	1596 VHIQHPNPAEATVQPLDLELTISSSLQPTAEGELLYSMQETVTQISEPPKQVVTPVPEYQ 1655 Qy	ପ୍ପ
2672 KSPEEMVSLSPKNKETVFPAQG	409	λŏ
	1536 VVAPVPVYQAVTVPTPSQYQAEYQKSLQPLDLELTVTSEPTKEAYHSTISKNSLAINPQY 1595 Qy	q _Q
 2613 BLTLSSQPHGWVPHHPNTPGKIN		ò
BLTB	1476 PMYIDVTLPQQVSVQHLKRPTEGIVQPLDLELTITPQPTPEGELSQTVQESTTQNKEPHKE 1535 Qy	ΩÞ
2553 LVKTTTKSKPAEWTPRRIDKLL	394	δλ
642TTPKEPAPTTP	1416 PTVVVGÞVPIYREVTVQTTSQDQABYPÞSPTVSPQSLDLGLTITPEPTEHFITQKTTVFP 1475 Qy	qa
: 2493 EDQDESPSPPNMSLKSLDQEVTM		Qy
621EEPAP	1357 TVHÞTKHPLVIHSBQTQHÞNPTEVTVQPLDLELTMTPQPTAEGELPQTLQDSTTQIIEP- 1415 Qy	qa
	356	δλ
584TPITPEKLAP	1297 IIEPPIKVVALVPVYQEVSQDQAEYTTSSTVSFQPLDQELTITSEAIREPHHPTVPQQTI 1356 Ov	qa
	318	ò
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: 2314 MSSQPHSGVPHPPKTPGKIYLHS	AKDLAPTSKV 286	δ
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	223KETTIN 252	ζ
506 TTPKEPSPTTTKEPAPTTPKEPA	1124 PLVIHSEQVYTQHPNPTEALIQPLDLELTITPQPTAEGELPQTLQDSTTQIIEPPTVVVG 1183	qu
2195 GESPSSPNMSLQSLDHELFMSSQ	203 NKVSTSPKITTAKPINPRPS	Λ0
	1064 PEHHEGTIPIPIQDQABYSTLPTVSFQPLDQBLTITSEAIREPPHPTVPQQTIIVHPPEH 1123 Qy	qu
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2075 MVSQSPKYEEAVLPVHGEGQEES	199	δλ
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: 1955 TTKSRPVQGTATQMAASPKBMVS	81 PSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEEHSVSEN 122	λΌ
461TPKE	850 ETTYNSKQVDLSSTHLKTSELPPDYTWGLEPSLYQQITQSSPKSLHENPKSFP 902 Qy	qa
: : : : 1896 ESQPPPNMSLQPLDQELTLSSQP	35 ESFERGRECDCDAQCKKYDKCCPDYESFCAEVH-NPTSPPSSKKAPP 80	ζŎ

SPEDRVSQTPEYKEAVLSGPGEDQDESPSPNMSLQSLD 2911 KIYLHYAEPPIGPFVEPPDLFFLKTTKSKPLQGTPTQMA 2971 : |:| GKGQDESPSPPNISLQSLDQEITMSSQPHGWIPHPPNTH 2731 FFLKTTKSKPMQGSPRQIDKSPKEMFTQSPEYEESLLPA 2791 BLSLSSHPHGWIPHHPNTPDKIYLHYAEPPTGPFVEPPD 2851 681 | : | | SRAPENKEAVLSGPGEDQDESPSPPNMSLQSLDQELTL 2014 KSKPVQGTATRMVKSPEEMVSLDPENKEAVFPAQGEGK 2194 QPHGWIPHPPKTPDKIYLHYAEPPTGPFVEPPDLFFLR 2254 ASIBPPGPFVKPTDLILVKTTTKSKPAEWTPRRIDKLL 2373 DESGSPPNMPLQPLDQELTLSSQPHGWVPHHPNTPGKI 2433 ----TTPKKP----- 692 727 ---APT--- 727 AEPPTGPFVEPPDLFFLKTTKSKPVEWTLTRTDKSRKE 2074 | : : | | SRSPPNMSLQSLEQELTLSSQPHGWVPHPPNTHGKIYL 2134 TTPEKPAPTTPEELAPTTPEEPTPTTP-------620 ---TTPKAAAPNTPK------EPAP------641 ---EPAP----- 564 ----- 496PITPKKL 583 ----KEPAP-----PAPTTP-------KKPAP-------KEPAPTTPK-ETA-----

	926	4112 GWITHPPNTPGKIYLHYABPPTGPFVEPPDLFFLKTTKSKPLAGTPTQMAKSPKEMFSQT 939	4172 LEHKEAVLSAPGEDQDESPSSSNMSLQSLDQDI	943KVTTTKK-TITTTEIMNKPEE	963	4,	968 D	4352 PVQMTPTQIDKSLKKNVAQSPEYERAVFPAHGEGQDESRYAPNISLGSLDHDITLSSQPH 4411	4412 GWIPHPPNTPDKIYLHYAEPPTGPFVEPPDLFFLKTKSKPAQWTPTPMAKSPBEMVSLS	981QK	; 4472 LKNKEAVLPAQGKDEEESISPPNMSLQPLDQELTLSSQPHGWVHHPPNTHGKIYLHYAEP 4531	983	4532 PTGPFVEPPDLFFLK	990TPT 1010 1	1011 PRKMTSTMPELNPTSRIABAMLQTTTRPNQTPNSKL	4652 KSPKEMVSQTPEYKEAVLSGEDLDESTSSPNMSLQPLDQELSLSSQPHGRIPHPVTSPGK 4711	1047	4712 IYLHYAEPP	1058 GAEGETPHMLLVTPDMD	1083	4832 FLKTTKSKPVQGTATQMAKSPEEMVSLSLENKEAVLPAQGDGLEESIFPPNMSLQPLDHE		4892	1121	4947 LIAKSPREMVSRSPEYKQALLPGHGEGKNESRSAPNMSLQPLDQELTMSS	1136 SPPSPARRITEVWGIPSPIDTVFTRCNCEGKTFFFFKDSQ	7000	11/5 - YWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYK	1213	TOPLDQELSLFSQP
KSPKEMVSQTPEYKEADLSAPGENRDESPSSPNMSLHPLDQELSLSSQPHGWIPHPPNTH 3031	Oy TTLKEP 748	GKIYLHYAEPPIGPFVEPPDLFFLKTITKSKPVQGSPSQIDKSPKEVFSQSPESEESVLPA 3091 Ov	OAEGOEESRAPHWSLQLLDOKLTLSSAPHGWIPHHPNTPGKIVIHYARDPTGPFVFDDD 3151		3211	FVEPPDLFFLRTTKSKPAQWTPTQWA 3271	VO 786	3331	GKIYLHYABPPTGPFVEPPDLFFLYTKSKPVOVSPROITDKSPFVFTPGSPFVFFGCFU.	A TIME		802	LFFLKTTKSKPVHGSPRQIDKSHKEMFTQSPEYEESVLPAQAEGQEESRAPPHMSLQPLD 3511		STPELSAEP	LDQDLTLSSHPHGWIPHHPNTP	854	DKIYLHYAEPPTGPFVEPPDLFFLKTTKSKPVHGSPRQIDKSPKEVFTQSPEYEESVLPA 3691	QY 0Y		LFFLKTTKSKPVHGSPRQIDKSPKEVFTQSPEYEESVLPAQAEDQEESRAPPHMSLQPLD 3811	876	QDLTLSSHPHGWITHHPNTHGKIYLHYAEPPTGPFVEPPDLFFLRTTKSKPVQWTPTQID 3871	888	KSREEMVSQSPENEEADIPRHGDGQDELRNPPIISLQPLDQELTLSSQPHGWVPHPPSTP 3931	OY TITAAPKMIKETATITE 905	DKIYLHYAEPPTGPFVEPPDLFFLRTTKSKPVQGTPTQLAKSPKEMVFQTPEYKEAVLSA 3991	VO 506 905 DP	PGEDQDETPSSPNMSLQSLDQELTMSSQPHGWLPHPPNTHGKIYLHYADPPTGPFVEPPD 4051	KITESK-ITATTTQVTSTTTQ
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Qy 1233 KQEPVQKCPGF	-GRRPA1246	δλ	₽ 4
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Qy 1247LNYLONY	PVYGEMIQVRRRFERA 1266	ò	469 TIKEPSPITPKEPAPTITKSAPTITKEPAPTITKSAPITPKEPSPITTKEPAPTITKEPA 528
: : S197 QPHGWIPHPPNTAGKIYLHYARPPTGPFVEPPDLFFLKTTKSKPVQGTATQSTQ	TTKSKPVQGTATQSTQ 5250	QQ	PPAPQVKSSPP
QY 1267 IGPSQTHTIRIQYSPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAI-	LPNVVTSAISLPNIR 1319	δλ	529 PTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTP 580
Db 5251SPKEI1SPSTRYK	: : : : -ISPSTRYKESVLTAAVVGQDESQSPPNIS 5284	qq	
QY 1320 KPDGYDYYAFSKDQYYNIDVPSRTARAITTRSGQTLSKVW 1359 Db 5285 LOPLDOELTLSSOPHVLISHPSSTNANTGHTLGKIY 5320	VW 1359 :: IY 5320	Qy Dp	581 KKLIPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPNT 635
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849915 extensin-like protein – maize O'snecies: Zea mays (maize)		3 &	
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A; Description: Pex genes: pollen-specific genes with A; Reference number: 849915	extensin-like domains.	DÞ	
A.Accession: 549915 A.Status: preliminary A.Molecule type: 100		λο qq	800 KPAPTTPETTPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPT 859
A; RESIDACES: 1-1100 CAUD. A; Cross-references: UNIPROT:Q41805; EMBL:Z34465; NID:g600117; PIDN:CAA84230	:g600117; PIDN:CAA84230.1; PID:g6001	ð	860 TKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQV 919
Query Match 12.3%; Score 898.5; DB 2; Best Local Similarity 20.5%; Pred. No. 1.7e-11;	Length 1188;	qa	: 1089 VKSPPPPAP 1097
Matches 278; Conservative 91; Mismatches	365; Indels 625; daps 55; OFTGCKEPPERERECTEROUM 47	٥y	
OY 6 LPIYLLLLISVEVI		QC	
48		දු ද	980 POKPTKAPKKPTSTKKFKTMPRVRKKTTPPPRKMTGTMPEINPISRIAEAMLGITIKKPN 1039
Db 346 NFSFAFNFFNSEAAVCMPSDKALVNLDDRDNCLGALRPAQKTALQCAPVLARPVDCSKH-	PAQKTALQCAPVLARPVDCSKH- 404	3 8	ı Ö
Qy 54 KCCPDXESFCABVHNPTSPPSSKKAPPPS	QTIKSTIKRSPKPPNKKK :	3 8	
405	SEPHT439	ò	1097 MLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDT 1156
OY TOWNIESEETTEEHSVOEROGESSSSSSSSSSSSTIMATASSANGELOAKLENAADIN Db 440VSPEPEPEPSV	4 4	QQ	IMAN
164 KNRTKKKPTPKP	C)	8 G	1157 VFTRCNCEGKTFFFKDSQYMRFTNDIKDAGYFKFIFKGF 1195
452	4 (
OY 216 PINPRPSLPPNSDTSKETSLTVNKETTVETKETTINKQI'SIDGKEKITISAKETQSLEKI Db 496 ASTPPPSL	503	B48666 cell pr	oliferation antigen Ki-67, short form - human
276	313	C;Speci C;Date: C;Acces R;Schlu	C;Species: Homo sapiens (man) C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 15-Mar-2004 C;Bates: 03-May-1994 #sequence_revision 03-May-1994 #text_change 15-Mar-2004 R;Schlueter, C.; Duchrow, M.; Wohlenberg, C.; Becker, M.H.G.; Key, G.; Flad, H.D.; Gerd
314	361	J. Cell A;Title	Biol. 123, 513-522, 1993 : The cell proliferation-associated antigen of antibody Ki-67: a very large, ubl
S62 PEKS	621	ins. A;Refer A;Acces	ence number: A48666; MUID:94043435; PMID:8227122 sion: B48666
OY 362 EPAPTTPKEPAPTTTKSAPTTP-KEPAPTTPKKPAPTTPKKPAPTT-F	414 SVKSSP 681	A;Statu A;Molec A;Resid	s: preliminary ule type: mRNA use: 1-2897 <sch> -references: EMBL:X6551</sch>

Similarity 12.3%; Score 897.8; DB 2; Length 2897; 4; Conservative 153, Mismatches 476; Indels 2023, Gaps MRT ———————————————————————————————————
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à	349 PITPKEPAPT383
qq	974 PQTPKEEAQALEDLIGFKELFQTPGHTEEAVAAGKTIKMPCESSPPESADIPTS 1027
Qy	384 TKSAPTTPKEPA 395
qu	:
ò	396 PITPKKDAPITPKEPAPITPKEPTPK 424
q _Q	1088 SVIGSKRHPKI-KEKAQPLEDLAGWKELFQTPVCTDKPTTHEKTTKIACRSQPDFVDTPT 1146
à	425 BPAPTIKE 436
d d	1147 SSKPQSKRSLRKVDVEEEFFALRKRTPSAGKAMHTPKPAVSGEKNIYAFMGTPVQKLDLT 1206
ζ	437pTAPKK 448
qa	1207 ENLTGSKRRLQTPKEKAQALEDLAGFKELFQTRGHTEBSMTNDKTAKVACKSSQPDLDKN 1266
ζ	449 PA
ପ୍ପ	1267 PASSKRRLKTSLGKVGVKEELLAVGKLTQTSGETTHTHTEPTGDGKSMKAFWESPKQILD 1326
ζζ	461EP TPKEPA
qu	1327 SAASLTGSKRQLRTPKGKSEVPEDLAGFIELFQTPSHTKE-SMTNEKTTKVSYRASQPDL 1385
٥٧	482APTTTKSAP
qu	: 1386 VDTPTSSKPQPKRSLRKADTEEEFLAFRKQTPSAGKAMHTPKPAVGEEKDINTFLGTPVQ 1445
δ	491SAPT 507
QQ	1446 KLDQPGNLPGSNRRLQTRKEKAQALBELTGFRELFQTPCTDNPTADEKTTKKILCKSPQS 1505
δŏ	508 PKEPSPTTKE 520
qa	
δ	521KKP 535
qa	1566 VEKLDLIGNLPGSKRRPQTPKEKAKALEDLAGFKELFQTPGHTEESMTDDKITEVSCKSP 1625
λo	536 APTIPKEPA 544
qq	1626 QPDPVKTPISSKQRLKISLGKVGVKEEVLPVGKLTQTSGKTTQTHRETAGDGKSIKAFKE 1685
۲۵ م	545PITPKEPAPTTPKEPA
අධ	1686 SAKQMLDPANYGTGMERWPRTPKEEAQSLEDLAGFKELFQTPDHTEESTTDDKTTKIACK 1745
ò	566 BPAPTTPKETAPTTPKKLTPTT
q	1746 SPPPESMDTPTSTRRPFKTPLGKRDIVEELSALKQLTQTTHTDKVPGDEDKGINVFRETA 1805
ζζ	588 PEKLAPTPEKPAPTTPBELAPTTPEEPTPTTPEEP 623
qu	1806 KQKLDPAASVTGSKRQPRTPKGKAQPLEDLAGLKELFQTPVCTDKPTTHEKTTKIACRSP 1865
à	624 AP 632
qq	 1866 QPDPVGTPTIFKPQSKRSLRKADVEEESLALRKRTPSVGKAMDTPKPAGGDEKDMKAFMG 1925
à	633
qq	1926 TPVQKLDLPGNLPGSKRWPQTPKERAQALEDLAGFKELFQTPGTDKPTTDEKTTKIACKS 1985
ζŏ	655 PAPTTPKET
du	1986 PQPDPVDTPASTKQRPKRNLRKADVEEEFLALRKRTPSAGKAMDTPKPAVSDEKNINTFV 2045

670	GTAPTILKEPAPITPKKPAPKELAPTITKEPTSTISDK 707 	
708	pap TTPKGTAPT 719	
2104	SCKSPQPESFKTSRSSKQRLKIPLVKVDMKEEPLAVSKLTRTSGETTQTHTEPTGDSKSI 2163	
720		
2164	KAFKESPKQILDPAASVTGSRRQLRTRKEKARALEDLVDFKELFSAPGHTEESMITUKNI 2223	
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2283		
790	PKEPAPTTPKKPAPTTPETPPPTSEVSTPTTTKEPTTIHKSPDESTPELSABPTP 845	
2343	TKIPCESPPLEVVDITASITKRHEKIKVQNVQNEEFSAV TRIQISGELLIGADARFAGENKALENSPKEPGVPTT	· <u>-</u>
2402	8	
876	DKTTERDLRTTPETTTAAPKMTKETALTTEKTTESKITATTTQVTSTTTQ 925	
2459	DKTTKIPCKSSPELEDTATSSKRRPRTRÄQKVEVKEELLAVGKLTQTSGETTHTDKEPVG 2518	
926	DITPEKITILKITILAPKVITIKKIITITEIMNKPEETAKPKDRA	,
2519	EGKGTKAFKQPAKRNVDAEDVIGSRRQPRAPKEKAQPLEDLASFQEL	
971		
2566	SQTPGHTEELANGAADSFTSAPKQTPDSGKPLKISRRVLRAPKVEFVGDVVSTRDPVKSQ	•
989	KPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNP 1 ::	
2626	SKSNTSLPPLPFKRGGGKDGSVTGTKRLRCMPAPEEIVEELPASKKQRVAP 2676	
1024	TSRIABAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLR	
2677	RARGKSSEPVVIMKRSLRISAKRIEPAEELNSNUMKINKEEHLLUSSSESSESSESSESSES 272	
1070	PHYEMPEVITEDMOYLPRYENQGIIINPMLSDETNICNGKPYDGLTTLRNGTLVAFRGHYF 1129 	
2724	VPE2740	
1130	WMLSPFSPPSPARRITEVWGIPSPIDIVFTRCNCEGKT 1167	
2741	EAEQQITEVFVLAERIEINRNEKKPMKTSPEMDIQNP2777	_
1168	FFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVYFFKRGGSI 1227	-
2778	2785	
1228	QOYIXXQEPUQKCPGRRPALNYPVYGEMIQVRRRREBRAIGPSQ 1271	
2786	:PRDKVTENKRCLRSARQNESSQPKVAEESGGQKSAKVLMQNQKGKGEAGNSD 2837	
1272	THTIRIQYSPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDY 1326	
2838	SMCLRSRKTKSQPAASTLESKSVQRVTRSVKRCAENPKKAED 2879	
1327	YAFSKDQ	
2880)NCVKKITTRS 2890	

T25697	ı
hypothetic	ical protein F16F9.2 - Caenorhabditis elegans e. Caenorhabditis elegans
C, Date: C, Access	15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 ion: T25697
R; Fulton submitte	., B. To the EMBL Data Library, August 1996 orion: The secuence of C. elegans cosmid F16F9.
A;Refere	
A;Status	: preliminary; translated from GB/EMBL/DDBJ
A;Residu A;Cross- A;Experi	ies: 1-1229 <ful> references: UNIPROT:Q94185; EMBL:U67956; PIDN:AAB07691.1; GSPDB:GN00028; CESP:F1 mental source: strain Bristol N2; clone F16F9</ful>
C;Geneti A;Gene: A;Map po	C;Genetics: A;Gene: CBSP:F16F9.2 A;Map position: A:Throne: 3s/1: 381/1: 482/2: 517/1: 971/1: 1021/2: 1179/3
A) INC. O.	ore 890.1: DB 2: Length 122
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qq	VVQSSSLLSKTINSDGSRDF
λŏ	61 SFCAEVHNPTSPPSSKKAPPPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEEHSVS 120
qu	57APSNPFDVSTTISSIN
δλ	121 ENQESSESSESSESSINWKIKSEKNSAANRELQKKLKVKDNKKNRTKK 169
qq	- B
ò	170 KPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKI 211
qo	121TISTDASTINAPITGKDSTIPELITGIVVINSKSESVT 158
ŏ	212TTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTNKQTSTDGKEKT 263
QQ	Ė
οχ	264 ISAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPAST 320
Dp	
ò	321 IPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTK 377
qa	EPTTTAESTTKKSTTKAPATT
ογ	43
QQ	290 ABTSTTTSSETSTBKPTTPLIDNKIAGPATGKPBTTHFFVTGTTFNFD 337
ζŏ	433 PAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAP 483
Db	338 TÄTETPEVAKSEDKMTLSKTAÅTETTQQTTEVT-DGPEKETTKNVSIEIPITTVPLVETT 396
'n	52
QQ	TESATTVKPFNEETTTKSHVVPKPTKKGTVKV 45
δλ	53
qq	457 TPKLELSFDEPTEIT-KAPHPGKLLEKKTYHFVLSDNFARYSEAKENDDYNHLDYNHYRE 515
δλ	
QQ	516 AKEPTITEESSTITEEVITTEEPANTGNPPITENPITTEQPISTAESTITALPFITEQ 572

TAPTIPKKLIPITEEKLAPITPEKPAPTIPEELAPITPEEPTPITPEEPAPTIPKAAAPN 634	TPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKE 691 :	TTPKGTAPTTLKE -:: VTESAITOTSVSV	RQLPERWKAIVNKFKHNLEVLKEKKRLIKEKESTITGSDSSRTTTKVPP		885	SAAFITGESPENTALQSSQKSEENESSAEKPGARRDFVPKKHKTTVKPAT	9 5 9 8 2 9	1002	TRPNOTPNSKLVEVN 1050	1063 1094	SINDEPER STREET	1158	1160	SVY 1219	1226	1221	1228
					TTIHKSPI : ST1	TPETTTA- : SETTTSE	TTESKITA : TSAVAAST	PEETAKPR	RKPKTTPT	HTTTD PKSEDAGG		QEQEIEEK	NGKPVDGL	CNCE-GKT	KNCEFAKR	FF 1221	AF 1228
575 573	635	692	748	770	826	886	907	960	1003	1051	1095	1099	1106	1161	1201	1220	1227
0y 20	oy G	y da	65 G	QY	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	oy Oy	& g	çy G	ý 5	සී රි සි	9 <i>&</i>	Ωp	oy Oy	δλ	qq	λō	අු

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mucin 1 precursor, repetitive splice form A [validated] - human
N.Alternate names: breast carcinoma-associated DF3 antigen; core protein KP39; episialin
ncreatic mucin; polymorphic epithelial mucin (PEM)
N.Contains: mucin 1 precursor, epithelial tumor antigen splice form; mucin 1 precursor,
C.Species: Homo sapiens (man)
C.Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #text change 02-Jun-2000
C.Accession: A35175; B35175; A35886; A35887; S10572; S40293; A36735; PX0066; S10218; SS1
N.Ligtenberg, M.J.L.; Vos, H.L.; Gennissen, A.M.C.; Hilkens, J.
D. Biol. Chem. 265, 5573-5578, 1990
```

A;Title: Episialin, a carcinoma-associated mucin, is generated by a polymorphic gene en A;Reference number: A35175; MUID:90202794; PMID:2318825

A; Accession: A35175

A; Accession: B35175

A; Accession: 1920.73
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A; Accession: 1920.73
A; Accession:

A,Status: not compared with conceptual translation

A Molecule type: mRNA

A Residues: 1-19,29-1109, 5',111-1339, 'A',1341-1344 < LAN>
A) Residues: 1-19,29-1109, 5',1111-1339, 'A',1341-1344 < LAN>
A) Residues: 1-19,29-1109, 5',1111-1339, 'A',1341-1344 < LAN>
A) Rocas-references: GB.J05582; NID:g189589; PIDN:AAA60019.1; PID:g189589
A;Note: GenBank entry HUMPANMU contains four fewer copies of the tandemly repeated sequing Wisconstructure, D.H.; Hareuveni, M.; Tsarfaty, I.; Smorodinsky, N.; Horev, J.; Zaretsky, J. Bur. J. Biochem. 189, 463-473, 1990
A;Title: Human epithelial tumor antigen cDNA sequences. Differential splicing may general systematic number: \$10571; MUID:90276413; PMID:2351132

A;Accession: S10572

A;Molecule type: mRNA A;Residues: 1-19,29-155,'P',157-175,'P',177-182,'A',184-212,1033-1344 <WRE> A;Cross-references: EMBL:X52229; NID:g37053

R;Wreschner, D.H. submitted to the BMBL Data Library, March 1990 A, Reference number: S40293 A, Accession: S40293

A; Molecule type: mRNA A; Mesiduas: 1-19,29-155, 'P',157-175, 'P',177-182, 'A',184-212,1033-1037,'A',1039-1344 < WR2 A; Cross-references: EMBL:X52229; NID:g37053; PIDN:CAA36478.1; PID:g37054 R; Abe, M.; Siddiqui, J.; Kufe, D Biochem. Biophys. Res. Commun. 165, 644-649, 1989 A; Title: Sequence analysis of the S' region of the human DF3 breast carcinoma-associated A; Reference number: A36735; MUID:90088473; PMID:2597151

A, Molecule type: mRNA

A/Residues: 1-142, 02',144-162,'0',164-168 cABE>
A/Cross-references: EMBL:M31823; NID:g181542; PIDN:AAA35757.1; PID:g181543
B. Mayauchi. 12: Hamanoue, M.; Ando, S.; Yoshida, J.; Takao, S.; Shimazu, H. R. Masuchem. 112, 609-615, 1992
A.Title: A novel core protein as well as polymorphic epithelial mucin carry peanut agglu A;Reference number. JX0235; MUID:93123189; PMID:1478919
A.Accession: PX0066
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A.Accession: PX0066
A.Accession: PX0066
A.Accession: BS., 1014-1017;1018-1032,'T',1034-1037;1038-1057 cAAS>
A.Experimental source: gastric carcinoma cell
R.Zrihan-Licht, S.; Baruch, A.; Elroy-Stein, O.; Keydar, I.; Wreschner, D.H.

A;Title: Tyrosine phosphorylation of the MUC1 breast cancer membrane proteins cytokine A;Reference number: S51026; MUID:95080414; PMID:7988707

A,Note: undetermined tyrosine residues in the carboxyl-terminal non-repetitive region ar C,Comment: This protein is length polymorphic. Individuals may have between 21 and 125 or partial repeats. The repeat shown is defined by Smal nuclease sites. A; Contents: annotation

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

OM protein - protein search, using sw model

Run on:

October 13, 2004, 11:23:49; Search time 109.728 Seconds (without alignments) 4449.477 Million cell updates/sec

SEQ1-G 7323 1 NAWKTLPIYLLLLLSVFVIQ.....ARAITTRSGQTLSKVWYNCP 1361 Title: Perfect score:

Scoring table:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.1

2002273 seqs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB

seq length: 0 seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_23Sep04:* Database

geneseqp2000s:*
geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:* geneseqp1980s:* geneseqp1990s:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Ad123265 Human MUC Abb69806 Drosophil Abb43908 MUCSB par Abu53255 Human tes Aag38942 Arabidops Abb61364 Drosophil Abb61364 Drosophil Abb68595 Drosophil Abb68397 Drosophil Abb60403 Drosophil	Abu53150 Human tes Abu53149 Human tes
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22222222222222244444444444444444444444	44

ALIGNMENTS

Megakaryocyte colony stimulating factor; secretion signal; meg-CSF; stability; proteolytic cleavage; adhesion; alternative splicing. AAR26049 standard; protein; 1404 AA. Location/Qualifiers 157. 200
| Jabel= Exon V | 200. 1141 | 14166. 1212 | 1166. 1213. 1266 | 1213. 1266 | 1213. 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1331 | 1266 | 1366 | 1366 | 1366 | 1366 | 1366 | 1366 | 13 /label= Exon_III 107. 157 /label= Exon_IV 1266. 1331 /label= Exon_X 26. 67 ___/label=_Exon_II 331. .1373 ____ label= Exon_XI 1. .26 /label_ Exon_I (revised)
(first entry) 67. .107 MSF precursor. 25-MAR-2003 02-FEB-1993 W09213075-A1 Synthetic AAR26049; Region Region Region Region Region Region Region Region Region Region Region Region

06-AUG-1992.

92WO-US000433. 17-JAN-1992;

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(GEMY ) GENETICS INST INC.
18-JAN-1991;
10-SEP-1991;
      Turner
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New human mega-karyocyte stimulating factors - for treating immune deficiencies, cancer, exposure to radiation or drugs, bacterial and viral infections, etc.
                                                                                                                                                                                                                             Claim 1, 2 and 3; Fig 1; 87pp; English
1992-284660/34
                                   N-PSDB; AAQ27223
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Gesner TG;

Hewick RM,

Jacobs K,

K, Clark SC,

91US-00643502.

The sequence given is a full length translation from the megakaryocyte stimulating factor (MSF) precursor. The sequence covered by exons II, III and III encodes megakaryocyte stimulating factor (MSF). This sequence is codified by the addition of an N-terminal sequence encoding a secretory leader, an initiating methionine proceeding exon II and a terminating codon following exon IV. The cDNA sequence given contains sequencess codon following exon IV. The cDNA sequence given contains the initiating methionine, and encodes a classical manualian protein secretion signal sequence. The sequence encoding the crision is protein secretion signal sequence. The sequence encoding the crision between amino acid residues 134 - 147. The primary transcript of this gene may be cleaved in different ways to yield a family of mRNA's cach encoding a different septement. Exons V and VI are thought to be cach encoding a different wist protein. Exons V and VI are thought to be stability, folding and processing of the molecule. These exons are also thought to play a role in the observed spnergy of MSF with other cytokines. Exons V - XII are believed to be implicated in the processing or folding of the appropriate structure of the resulting factor, ie. one corn more of these exons may contain sequences which direct proteolytic matrix processing. Both naturally occuring and non-naturally occuring matrix processing. Both naturally occuring and non-naturally occuring spliced exons from this sequence, with the exons spliced together in differing orders to form different members of the MSF family. (Updated on differing orders to form different members of the MSF family. (Updated on the correct PN field.)

Sequence 1404 AA;

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156 257 300 TIPKEPITIIKSAPITIKEPAPITIKSAPITIPKEPAPITIKEPAPITIKEPAPITIKEP 377 120 120 180 240 9 TQHNKVSTSPKITTAKPINPRPSDPNSDTSKETSLTVNKETTVETTTTNKQTSDG KRVCTAELSCKGRCFESPERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP TQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTNKQTSTDG KEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPAS --VKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTST MAWKTLPIYLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF Gaps DB 2; Length 1404; . 43; Indels Score 7308.7; DB 2; Pred. No. 1.8e-176; 0; Mismatches 0; PPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITE-; 0 99.8%; Query Match
Best Local Similarity 96.9
Matches 1361; Conservative 241 258 301 318 181 198 Н 61 121 121 157 61

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1037 1097 1140 1157 1200 1217 1260 1277 1320 1337 1380 737 780 797 840 900 917 960 977 099 677 720 857 420 557 009 617 APTTIKSAPITIPKEPAPITIPKKPAPITIPKEPAPITIPKEPITITPKEPAPITKEPAPITIPK 480 EPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPT 497 RCNCBGKTFFFKDSQYWRFTND1KDAGYPKP1FKGFGGLTGQ1VAALSTAKYKNWPESVX SPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYYAFSKDQYXNIDV SPARLAYODKGVLHNEVKVSILWRGLPNVTSAISLPNIRKPDGYDYYAFSKDQYYNIDV QTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLS TSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPK QTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLS DETINICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFT 1141 DETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPFSPARRITEVWGIPSPIDTVFT 1201 RCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVY FFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRRFERAIGPSQTHTIRIQY **PBEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEP** APTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKGPAPTTPKG APTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKG TAPITLKEPAPITPKKPAPKELAPITTKGPISTISDKPAPITPKETAPITPKEPAPITPK KPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPT KPAPTTPETTPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPT **TKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQV** POKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPN **APTITKSAPTIPKEPAPTIPKKPAPTIPKEPAPTITPKEPTPTIPKEPAPTITPK EPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKSPAPT** TTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKP APTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTT PSRTARAITTRSGOTLSKVWYNCP 1361 PSRTARAITTRSGQTLSKVWYNCP 1404 1278 1338 1381 1158 1218 841 1021 1038 901 961 978 1081 1098 198 858 918 541 661 678 738 781 378 421 438 481 498 601 618 721 361 558 g 셤 g g à qq ò P ò 셤 ð à ð a ò 셤 à ð g q ò Db ò gg à 셤 δ q 8 à à g ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a human tribonectin which is a product of alternative splicing of the human MSF (megakaryocyte stimulating factor) gene. The tribonectin has at least one O-linked oligosaccharide lubricating moiety and has a polypeptide sequence comprising 1-76 repeats of a motif having at least 50% identity to the sequence KERPAPT (AAR2974). The invention also relates to a nucleic acid encoding a human KSF-derived tribonectin; a biocompatible composition comprising a human tribonectin for inhibiting tissue adhesion formation; and a method of masuring the amount of MSF compared to osteoarthritis by mammal, wherein an increased amount of MSF compared to a control confidence the presence of or predisposition to developing osteoarthritis. The tribonectin and DNA encoding it are useful in the treatment of costeoarthritis, where they may be used for lubricating mammalian joints, when formulated as a membrane, foam, gel or fibre, is useful for such as articulating joints of humans, dogs or horses. The tribonectin, where the injury is caused by a surgical insertion or trauma, or mammal, where the injury is caused by a surgical insertion or trauma, or has ential ficial device e.g., an orthopaedic implant. In particular, one of the ential and ential and ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ential ent
                                                                                                                                                                                                                                Human MSF; megakaryocyte stimulating factor; tribonectin; alternative splicing; joint boundary lubricant; 0-linked oligosaccharide; osteoarthritis; tribosupplementation; tissue adhesion inhibition; friction coefficient reduction; gene therapy; antiarthritic; osteopathic.
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                                                                                                                                                                              Human megakaryocyte stimulating factor (MSF), SEQ ID NO:1.
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                           standard; protein; 1404
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CC COXA vara-perioariditis (GACP) protein.

The composition may further comprise a local anaesthetic. The composition of the invention may be administered via intra-articular or intravenous of the invention may be administered via intra-articular or intravenous injection. The buman CACP protein is identified in the invention as being megakaryocyte stimulating factor (MSF). The gene encoding CACP protein (MSF) is located on chromosome 1q25-31, and mutations in this gene are creponsible for the heritable disorder camptodactyly—arthropathy-coxa vara-perioarditis, in which patients have synovial hyperplasia without evidence of inflammation. CACP protein (MSF) acts as a synovium confidence of inflammation. CACP protein (MSF) acts as a synovium creatment of osteoarthritis (e.g., joint pain, loss of range of movement symptoms of osteoarthritis (e.g., joint pain, loss of range of movement of osteoarthritis (e.g., joint pain, loss of range of movement of ortion damage). The present sequence represents human megakaryocyte crimilating factor (MSF, CACP protein). Note: This sequence is not given contained in its entirety in figure 4 of the specification, although a GenBank contained from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, CACP protein; camptodactyly-arthropathy-coxa vara-pericarditis; MSF; megakaryocyte stimulating factor; synovial lubricant; chromosome 1q25-31; osteoarthritis; joint lubrication; osteopathic;
  RCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVY
                                        FFKRGGSIQQY1YKQEPVQKCPGRRPALNYPVYGEMTQVRRRFERAIGPSQTHTIRIQY
                                                                    SPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYYAFSKDQYYNIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New composition comprising the camptodactyly-arthropathy-coxa varapericarditis protein in combination with an anesthetic, useful for treating osteoarthritis, or as lubricants of tissue and joints.
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2000US-00145328.
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                                                                           KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP
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                                                                                                                                                                                                                                                                                               TQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTNKQTSTDG
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Score 7308.7; DB 4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New tribonectin polypeptides and polymucleotides for lubricating joints or other tissues to prevent or treat Camptodactyl-arthropathy-pericarditis syndrome or osteoarthritis.
                            DETINI CNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFT
                                                                                                                                                                                                                                                                                                    FFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRFERAIGPSQTHTIRIQY
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                                                                              QTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLS
                                                                                                                                                                                  RCNCEGKTFFFKDSQYWRFTNDIXDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lubricating polypeptide; O-linked oligosaccharide; joint lubrication; CAP; camptodactyl-arthropathy pericarditis; osteoarthritis; human; megakaryocyte stimulating factor; MSF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genetic
                                                                                                                                                                                                                                                                                                              SPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYYAFSKDQYYNIDV
                                                                                                          RCNCEGKTFFFKDSGYWRFTNDIKDAGYPKPIFKGFGGLTGGIVAALSTAKYKNWPESVY
                                                                                                                                                                                                                                                                     PFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRRFERAIGPSQTHTIRIQY
                                                                                                                                                                                                                                                                                             SPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYYAFSKDQYYNIDV
POKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIABAMLQTTTRPN
                                                              POKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPN
                                                                                          QTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLS
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                                                                                                                                                                                           RCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVY
                                                                                                                                                                                                                                             PFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRRFERAIGPSQTHTIRIQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used proliferation; to regulate haematopoissis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or simulation; as anti-inflammatory agents; and in treatment of leukaemias. AA(229510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention
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                                                                                                                                                        The invention relates to a method of determining the angiogenic index of a tissue or cell sample comprising assessing, in a sample, the expression levels of one or more differentially-expressed gene from any of 34 DNA sequences, given in the specification, where the levels are indicative the angiogenic index. The methods and compositions of the present invention are useful for diagnosing preventing and/or treating cancer, coronary artery disease, myocardial ischemia or coronary artery disease, myocardial ischemia or coronary arteriosclerosis. They can also be used in research, drug discovery and forensic medicine involving angiogenesis. This sequence corresponds to one of the differentially expressed proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTFTPKEPAS
                                                                                                                                                                                                                                                                                                                                                                                                                            KRVCTABLSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 KIKSSKNSAANRELQKKLKVKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTNKQTSTDG
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                                                      Determining the angiogenic index of a tissue or cell sample using expression levels of differentially expressed genes, useful for diagnosing or treating cancer, coronary artery disease, myocardial
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                                                                                                                                                                                                                                                                                                                                                    Length 1404;
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                                                                                                                                                                                                                                                                                                                                                  Score 7293.7; DB 7;
Pred. No. 4.2e-176;
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Matches 1358; Conservative
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                                                                                                                                                              SPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYXAFSKDQYYNIDV
                                         APTTPKKPAPKELAPTTTKEPTSTTCDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKG
                                                                                    TAPTITKEPAPTIPKKPAPKELAPTITKGPISTISDKPAPTIPKETAPTIPKEPAPTIPK
                                                                                                                       KPAPTTPETPPPTPPPTTSEVSTPTTTKEPTTTHKSPDESTPELSAEPTPKALENSPKEPGVPT
                                                                                                                                                                                           TSTTTQDTTPFKITTLXTTTLAPKVTTTKKTITTTBIMNKPEETAKPKDRATNSKATTPK
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                                                                                                                                                                                                                                                QTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLS
                                                                                                                                                                                                                                                                                            QTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLS
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PEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTLKEP
                              APTIPKKPAPKELAPTITKEPISTISDKPAPTIPKGTAPTIPKEPAPTIPKEPAPTIPKG
                                                                     TAPITLKEPAPITPKKPAPKELAPITTKGPTSTTSDKPAPITPKETAPITPKEPAPITPK
                                                                                                             KPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Determining the angiogenic index of a tissue or cell sample expression levels of differentially expressed genes, useful
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                                                             2002US-00067482.
2002US-00164595.
2002US-0403649P.
2003US-0437746P.
2003WO-US003848
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N-PSDB; ADK65818.
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16-AUG-2002; 2
03-JAN-2003; 2
      07-FEB-2003;
                                                                 07-FEB-2002;
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ADK67912 standard; protein; 1311 (first entry) RESULT

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(EXMES) polypeptide. Human extracellular messenger

Human; extracellular messenger; EXMES; respiratory-gen.; antiallergic; antiasthmatic; antiinflammatory; antidiabetic; neuroprotective; muscular-gen.; antiarthritic; osteopathic; hepatotropic; antipsoriatic; virucide; fungicide; antiparasitic; protozoacide; antihelminthic; cytostatic; gene therapy.

New extracellular messengers and nucleic acids, useful for diagnosing, tracating or preventing e.g. allergies, anemia, Crohn's disease, diabetes mellitus, myasthenia gravis, osteoporosis, psoriasis, cancers or autoimmune thyroiditis. 30 ь .. , JP; Ramkumar J or 29 24, ure R, Tran UK, Swarnakar A, Marquis J Emerling BM, Lindquist EA, Chawla NK, 21, /note= "Spans residues 1 to 18, 20, according to identification method" 1. .30 /label= Signal_peptide /note= "Spans residues Location/Qualifiers 2002US-0400810P. 2002US-0412197P. 2002US-0416004P. 2002US-0424862P. 2003WO-US024084 WPI; 2004-157116/15. N-PSDB; ADK67917. (INCY-) INCYTE CORP. Khare Elliott VS, Kha Richardson TW, Lee SY; WO2004013292-A2 02-AUG-2002; 19-SEP-2002; 04-OCT-2002; 30-JUL-2003; 08-NOV-2002; 12-FEB-2004 Peptide Key

The present sequence is that of novel human extracellular messenger
(EXMES) Incyte ID NO: 7513018CD1 polypeptide. The protein shows homology
to human megakaryocyte stimulating factor. The invention provides EXMES
polymucleotides and polypeptides, as well as expression vectors, host
cells, antibodies, agonists and antagonists, and methods for diagnosing,
treating or preventing disorders associated with aberrant expression of
EXMES, especially autoimmune and inflammatory disorders, cell
proliferative disorders and endocrine disorders, e.g. adult respiratory
distracts syndrome, allergy, anaemia, erythroblastosis foetalis, Crohn's
distracts mellitus, myasthenia gravis, osteoarthritis,
osteoporosis, pancreatitis, psoriasis, viral, bacterial, fungal,
parastic, protozoal or helminthic infections, cancers, autoimmune
thyroiditis, cretinism, Plummer's disease or thyroid carcinoma.
Embodiments also provide methods for using the purified EXMESs and/or
their encoding polymucleotides for facilitating the drug discovery
process, including determining of efficacy, dosage, toxicity and
pharmacology, and for investigating the pathogenesis of diseases and
medical conditions. Claim 60; SEQ ID NO 5; 165pp; English

Sequence 1311 AA;

ή: 120 9 9 1 MAWKTLPIYLLILSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCOHYMECCDFF MAWKTLPIYLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF KRVCTABLSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP Gaps 50; Length 1311; 61 KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCA----Indels Score 7043; DB 8; Pred. No. 8.4e-170;); Mismatches 1; ; 96.2%; Query Match
Best Local Similarity 96.3
Matches 1310; Conservative 61

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The present sequence is that of novel human extracellular messenger (EXMES) Incyte ID NO: 7513017CD1 polypeptide. The protein shows homology to human megakaryocyte stimulating factor. The invention provides EXMES polynucleotides and polypeptides, as well as expression vectors, host cells, antibodies, agonists and antagonists, and methods for diagnosing, treating or preventing disorders associated with aberrant expression of EXMES, especially autoimmune and inflammatory disorders, cell proliferative disorders and endocrine disorders, e.g. adult respiratory distances syndrome, allergy, anaemia, erythroblastosis foctalis, Crohn's disease, diabetes mellitus, myasthenia gravis, osteoarthritis, osteoporosis, pancreatitis, psoriasis, viral, bacterial, fungal, charolitic, protozoal or helminthic infections, cancers, autoimmune thyroiditis, cretinism, Plummer's disease or thyroid carcinoma.
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19-SEP-2002; 2002US-0412197P.
04-OCT-2002; 2002US-0416004P.
08-NOV-2002; 2002US-0416004P.
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/label= Signal peptide
/note= "Spans residues 1 to 18, 20,
according to identification method"
                                                                                                           GYDYYAFSKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP
                                                                                   GYDYYAFSKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP
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their encoding polynucleotides for facilitating the drug discovery process, including determining of efficacy, dosage, toxicity and pharmacology, and for investigating the pathogenesis of diseases and medical conditions.
                                                                                                   Gaps
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Pred. No. 3.9e-163;
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1080 1140 1049 1260 1169 1320 1229 Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; PTSRIABAMLOTTTRPNOTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMD TAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELN PISRIABAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMD YLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPAR YLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPAR 1110 VAALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGETIQVRRRRR TIEKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTEIMNKPEE RITEVWGIPSPIDIVFTRCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGGLTGG VAALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRR PERAIGPSQTHTIRIQYSPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPD RITEVWGIPSPIDIVFTRCNCEGKTFFFKDSQYWRFTWDIKDAGYPKPIFKGFGGLTGQI raising ; Asundi Isolated polypeptide for treatment of diseases, diagnostics, antibodies and research use. GYDYYAFSKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP 1361 Ŗ, Chen ž Human EST encoded protein SEQ ID NO: 1847. Wang Page 1198-1201; 1275pp; English Qian XB, Wa J, Werhman Ā protein; 1299 2000US-00491404. 2000US-00617746. 2000US-00631451. 2000US-0063870. 25-JAN-2001; 2001WO-US002687 Zhou P, (A, Zhang (first entry) gene therapy; nutrition. Liu C, Zh Drmanac RA, WPI; 2001-476164/51. N-PSDB; AAH98981. standard; (HYSE-) HYSEQ INC WO200154477-A2. 25-JAN-2000; 17-JUL-2000; 03-AUG-2000; 15-SEP-2000; sapiens 12-OCT-2001 02-AUG-2001 1050 1201 1141 1261 810 870 1021 930 1081 066 1321 Claim 20; 1230 961 AAM24322 AAM24322, rang YT, Homo RESULT 10 g g g ⋩ ò ð à g ò qq g g ò ð

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                                                                                                                                                                             Gaps
proteins from a variety of organisms, including human, dog, cat, hor cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a
                                                                                                                                                                           43;
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                                                                                                                                             Score 6732.7; DB 4
Pred. No. 5.9e-162;
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1080 1140 1157 1217 1260 a human human 1097 1020 1037 096 716 Human tribonectin, MSF, megakaryocyte stimulating factor, alternative splicing, joint boundary lubricant, 0-linked oligosaccharide, osteoarthritis, tribosupplementation; tissue adhesion inhibition, friction coefficient reduction; gene therapy, antiarthritic, osteopathic. TSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPK TSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTBIMNKPBETAKPKDRATNSKATTPK POKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPN POKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPBLNPTSRIABAMLQTTTRPN QTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLS DETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFT DETNICHGERPUNGLITHENGTLVAFRGHYFWMLSPFSPARRITHEVWGIPSPINTVFT RCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVY RCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVY The invention relates to a human tribonectin which is a product of alternative splitching of the human MSF (megakaryocyte stimulating figure. The tribonectin has at least one 0-linked oligosaccharide lubricating moiety and has a polypeptide sequence comprising 1-76 of a motif having at least 50% identity to the sequence KRPAPTT (AAB2977A). The invention also relates to a nucleic acid encoding MSF-derived tribonectin, a biocompatible composition comprising a treating Novel tribonectin polypeptide useful as lubricant for osteoarthritis, comprises O-linked lubricating moiety ISLAND HOSPITAL LIFESPAN PARTNER FFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGE FFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGE Ą Disclosure; Fig 1; 47pp; English. AAB29778 standard; protein; 902 Human MSF-derived tribonectin. 2000WO-US010953. (first entry) WPI; 2001-024673/03. osteoarthritis, WO200064930-A2 (RHOD-) RHODE sapiens. 24-APR-2000; 23-APR-1999; 28-FEB-2001 02-NOV-2000 1021 1098 1141 1158 1201 1218 1261 AAB29778; 196 1038 901 918 978 1081 858 8 Homo RESULT 11 Jay AAB2977 q 원 g δ g ò d à 임 ò ð g ð

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tribonectin for inhibiting tissue adhesion formation; and a method of diagnosing osteoarthritis or a predisposition to osteoarthritis by measuring the amount of MSF or its fragment in a biological sample of a mammal, wherein an increased amount of MSF compared to a control indicates the presence of or predisposition to developing osteoarthritis. The tribonectin and DNA encoding it are useful in the treatment of osteoarthritis, where they may be used for lubricating mammalian joints, such as articulating joints of humans, dogs or horses. The tribonectin, when formulated as a membrane, foam, gel or fibre, is useful for inhibiting adhesion between two surfaces such as the injured tissues of a mammal, where the injury is caused by a surgical insertion or trauma, or an artificial device e.g., an orthopaedic implant. In particular, one of the surfaces is pericardial tissue. DNA encoding a tribonectin may be used in gene therapy. The present sequence represents a substantial portion of a human MSF-derived tribonectin.

Sequence 902 AA;

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PRPSLPPNSDISKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAK 276 PRPSLPPNSDTSKETSLTVNKETIVETKETTTINKQTSTDGKEKITSAKETQSIEKTSAK 120 DLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTTTIKSAPTTPK 336 516 335 576 989 440 969 DLAPTSKVLAKPTPKAETTTKGPAL-----TTPKEPASTTPKEPTTTKSAPTTPK 172 РККРАРТТРКЕРАРТТРКЕРТРТТРКЕРАРТТКЕРАРТТРКЕРАРТАРККРАРТТРКЕРА 456 EPTSTISDKPAPITPKGTAPITPKEPAPITPKEPAPITPKGTAPITLKEPAPITPKKPAP 756 541 814 595 872 932 667 VKDNKKNRIKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTGTTQHNKVSTSPKITTAKPIN 60 157 VKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPIN **EPAPITIKSAPITIPKEPAPITIKEPAPITIPKEPAPITIKEPAPITIKSAPITIPKEPAPIT** PTTPKEPAPTITKEPSPTTPKEPAPTITKSAPTITKEPAPTITKSAPTTTKEPSPTTTKE PTT-KEPAP-TTKEPAPTT-KEPAPTTKEPAP-TTKEPAPTTKEPAPTT-KEPAP-TTKE PAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTKKPAPTAPKEPAPTTPKETAPT **TPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPNTPKE** PAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTK --KELAPTITKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEV TTKEPAP-TTKEPAPTTKE-PAPTT-KEPAPTT-KEPAPTTKE-PAPTTKE STPITIKEPITIHKSPDESTPELSAEPTPKALENSP--KEPGVPITKTPAATKPEMTITA 873 KOKITERDIRTIPETITIAAPKMIKETAITIEKITESKITAITIQVISITIQDITPFKITI ---TKEPAPTT-----KEPAPTTKEPAPTTKEPAP----A--PITKEPAPITKEPAPIT----KEPAPITKEPAPITKEP-APITKEPAPI Conservative Similarity 795; 441 Query Match Best Local S 217 61 121 229 542 277 337 173 397 457 282 517 336 577 389 637 697 489 757 815 641 Matches

TLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFTRCNCEGKTFFFKDSQ 1172 TLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDIVFTRCNCEGKTFFFKDSQ 855 KPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIABAMLQTTTRPNQTPNSKLVEVNPKSE 933 LKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKRPTSTK -----TTKEPAPTTKEP-APT-TK -----APTIPTERMISTMPELNPTSRIAEAML-TTTRPNOTPNSKLVEVNPKSE DAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLT DAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLT YWRFINDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVYFFK 1220 YWRFINDIKDAGYPKPIFKGFGGLIGQIVAALSTA-YKNWPESVYFFK 902 Human testes-derived DKFZphtes3_4019 homologue Example III; Page 892-893; 1095pp; English. (GEHU-) GERMAN HUMAN GENOME PROJECT Æ ABU53253 standard; protein; 551 99US-0156503P 99US-0149499P (first entry) Nucleic acids having the different human tissues, WPI; 2001-327840/34. of a polypeptide Sequence 551 AA; WO200112659-A2 Homo sapiens 18-AUG-2000; 18-AUG-1999; 28-SEP-1999; EP 14-APR-2003 22-FEB-2001 ŝ 993 685 1053 736 1113 961 1173 Query Match RESULT 1 ABU53253 Q à g à g δ g ð 염 48.5%; Score 3552; DB 4; Length 902; 74.4%; Pred. No. 1e-81; ive 27; Mismatches 76; Indels 170;

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from human cDNA libraties which can be used for gene therapy or in vaccines. The polymucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue This invention describes novel polynucleotides and polypeptides isolated sequences of clones isolated from libraries of useful in recombinant DNA methodologies. described in the disclosure of the invention Human; gene therapy; vaccine; disease treatment; detection.

Gaps .; Indels 40.0%; Score 2929; DB 4; 100.0%; Pred. No. 2.9e-66; ive 0; Mismatches 0; Best_Local Similarity 100. Matches 551; Conservative

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from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention
                               describes novel polynucleotides and polypeptides isolated
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Example III; Page 892; 1095pp; English
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                                                                                                                                                                 LKEPAPITPKKPAPKELAPITIKEPISITSOKPAPITPKGTAPITPKEPAPITPKEPAPI
                                                                                                                                                                                                                             TPKGTAPTTLKEPAPTTPKKPAPKELAPTTKGPTSTTSDKPAPTTPKETAPTTPKEPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRPNOTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNOGIIIN
                                                                                                                                                                                                                                                                                                                                                                                                                            TIQVISTITIQDITPFKITILKTITLAPKVITTKKTITITEIMNKPEETAKPKDRAINSKA
   TKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEP
                   TKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEP
                                                                                      TPTTPEEPAPTTPKAAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTT
                                                                                                                                   LKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPT
                                                                                                                                                                                                      TEKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAP
                                                                                                                                                                                                                                                                       TIPKKPAPTTPETTPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEP
                                                                                                                                                                                                                                                                                                 TTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEP
                                                                                                                                                                                                                                                                                                                                        GVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITAT
                                                                                                                                                                                                                                                                                                                                                                       GVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTPKPOKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIABAMLQTT
                                                                  TPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy; vaccine; disease treatment; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human testes-derived DKFZphtes3_4019 homologue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-AUG-1999;
28-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAF 1122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences of human superficial zone protein (SZP). The protein is involved in the lubrication of joints, and the sequences can be used in the treatment of degenerative joint conditions or to delay symptoms of a degenerative joint condition, e.g. osteoarthritis, rheumatoid arthritis, gout, psoriatic arthritis, reactive arthritis, wiral or post viral arthritis, spondylarthritis, juvenile arthritis, sprovitis, tendonitis, systemic lupus erythematosus, CACP, osteoporosis or trauma. The present sequence is the protein encoded by the human 3' cartilage SZP cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                      New purified superficial zone protein (SZP) polypeptides, useful for treating degenerative joint conditions, e.g. osteoarthritis, rheumatoid arthritis, gout, spondylarthritis, synovitis, tendonitis, lupus, or osteoporosis.
antirheumatic; osteopathic; antigout; antiinflammatory; dermatological; immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HMLLRPHVFMPEVTPDMDYLPRVPNQGIINPMLSDETNICNGKPVDGLTTLRNGTLVAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMITTAKDKTTERDLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETP
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                                                                                                                                                                                                                                                                                                         Kuettner KE, Schmid TM, Schumacher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2850.9; DB 5
Pred. No. 2.6e-64;
); Mismatches 0;
                                                                                                                                                                                                                                                           GLAXO GROUP LTD.
RUSH PRESBYTERIAN ST LUKE MEDICAL CENT
                                                                                                       /note= "encoded by ACTACT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 59; Page 86-87; 89pp; English.
                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.9%;
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                                                                                                                                                                                                                              29-DEC-2000; 2000US-0258920P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         538; Conservative
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Best Local Similarity
Matches 538; Conserv
                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAL49079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 538 AA;
                                                                                       Misc-difference
                                                                                                                                       WO200262847-A2
                                                                                                                                                                                                                                                                                                         Hutchins JT,
                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                         Dixon EP;
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PALNYPVYGEMTQVRRRFFERAIGPSQTHTIRIQYSPARLAYQDKGVLHNEVKVSILWRG 1302 AGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRR 1242 419 from human cDNA libraries which can be used for gene therapy or in the wacdines. The polymocleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention 0 LPNVVTSAISLPNIRKPDGYDYYAFSKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP 1361 283 61 NSDISKETSLIVNKETIVETKETTINKQISIDGKEKTISAKETQSIEKTSAKDLAPISK 120 284 VLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTTTIKSAPTTPKEPAPTTT 343 9 LPNVVTSAISLPNIRKPDGYDYYAFSKDQYYNIDVPSRTARAITTRSGGTLSKVWYNCP 538 This invention describes novel polynucleotides and polypeptides isolated Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies. 420 PALNYPVYGEMTQVRRRRFERAIGPSQTHTIRIQYSPARLAYQDKGVLHNEVKVSILWRG AGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRR RIKKKPIPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPP 1 RIKKKPIPKPPVVDEAGSGLDNGDFKVTIPDISTIQHNKVSTSPKITTAKPINPRPSLPP NSDISKETSLIVNKETIVETKETITINKQISIDGKEKTISAKETQSIEKTSAKDLAPISK .; 0 513; Human; gene therapy; vaccine; disease treatment; detection. Indels Length Human testes-derived DKFZphtes3_4019 homologue #3. Score 2757; DB 4; Pred. No. 5.8e-62; 0; Mismatches 0; Example III; Page 893; 1095pp; English. PROJECT Ā 37.6%; Sco 100.0%; Pro tive 0;) 513 2000WO-IB001496. 99US-0149499P. 99US-0156503P (GEHU-) GERMAN HUMAN GENOME standard; protein; Conservative (first WPI; 2001-327840/34. Local Similarity Sequence 513 AA; WO200112659-A2. Homo sapiens 18-AUG-2000; 18-AUG-1999; 28-SEP-1999; 513; 14-APR-2003 22-FEB-2001 ŝ 360 1243 1303 224 1183 480 ABU53254 ABU53254; Query Match Wiemann Best Loca RESULT 15 g a à qq a ò g à δ 8

	KSAPTTPKEPAPTTPKKPAPT 403		APKKPAPTTPKEPAPTTPKEP 463		PTTPKEPSPTTTKEPAPTTPK 523		KEPAPITPKETAPITPKKLTP 583	KEPAPTTPKETAPTTPKKLTP 420	PITPKAAAPNTPKEPAPITPK 643			
	KSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTT	. KSAPITTPKEPAPITIKEPAPITTPKEPAPITIKEPAPITTKSAPITTKSAPITTPKKPAPI	TPKEPAPITPKEPIPITPKEPAPITKEPAPITPKEPAPITPKEPAPITPKEPAPITPKEPAPITIPKE	TPKEPAPTTPKEPAPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTPKEP	APTITKEPSPITFKEPAPTITKSPAPTITKEPAPTITKEPAPTITKEPAPTITKEPAPTITK	. APITIKEPSPITIPKEPAPITIKSAPITIKEPAPITIKSAPITIPKEPSPITITEPAPITIPK	EPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKKTPP	BPAPTTPKKPAPTTPKBPAPTTPKBPAPTTTKKPAPTAPKEPAPTTPKETA	TIPEKLAPTIPEKPAPTIPEELAPTIPEESPIPITPEEPAPTIPKAAAPNIPKEPAPTIPK	TTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPT	BPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKE 676	
121	344	181	404	241	464	301	524	361	584	421	644	481
q	δλ	qq	δ	qu	δλ	qq	٥٧	Db	δλ	qu	ð	qq

Search completed: October 13, 2004, 11:37:22 Job time: 116.728 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

October 13, 2004, 11:23:49 ; Search time 23.6582 Seconds (without alignments) 3815.116 Million cell updates/sec Run on:

SEQ1-G 7323

1 MAWKTLPIYLLLLSVFVIQ......ARAITTRSGQTLSKVWYNCP 1361 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.1 **BLOSUM62** Scoring table:

478139 seqs, 66318000 residues Searched:

478139 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Issued Patents AA: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		℀			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
н	7323	100.0	Н	4	US-07-757-022B-40	Sequence 40, Appl
7	30	9	1404	4	- 1	2
Э	308	٠	П	4	US-07-757-022B-62	equence 62,
4	7308.7	99.8	٦	4	-09-298-	Н
S	7293.7	9.	140	4	US-10-164-595-78	78,
9	7084.3	ė.	7	4	US-07-757-022B-48	48,
7	7058.9	96.4	П	4	US-07-757-022B-46	46,
6 0	7058.9	96.4	_	4	-07-757-022B-6	60,
σ	7049	9	-	4	US-07-757-022B-42	equence 42;
10	044.		П	4	-07-757-022B-	52,
11	7043.9	96.2	Н	4	US-10-164-595-58	58
12	836	93.4	Н	4	9	50
13	820.	93.1	1313	4	-07-757-022B-	142,
14	784	92.7	Н	4	US-07-757-022B-44	4
15	86		٦	4	US-07-757-022B-104	equence 104,
16	5485.7			4	US-07-757-022B-74	74.
17	5472		П	4	-07-757-	equence 84,
18	5379.2	73.5	-	4	US-07-757-022B-58	equence 58,
19	5011	68.4	941	4	-07-757-	14,
20	2246.2	30.7	4	4	US-07-757-022B-54	54,
21			423	4	-07-757-	99
22				4	US-07-757-022B-68	68,
23				4	US-07-757-022B-64	64
24	13.		5179	4	US-09-538-092-1258	equence
25	σ			4	US-07-757-022B-70	70.
26	1214.6	16.6		4	US-07-757-022B-72	equence 7
27	α		80	4	US-08-714-741-32	equence 32,

Sequence 116, App		30,	Sequence 32, Appl	94	Sequence 132, App	Sequence 92, Appl	90	Sequence 88, Appl	1, A	Sequence 106, App	Sequence 118, App	٠.	Sequence 114, App	Sequence 2, Appli	Sequence 98, Appl	Sequence 22, Appl
US-07-757-022B-116	US-07-757-022B-96	US-07-757-022B-30	US-07-757-022B-32	US-07-757-022B-94	US-07-757-022B-132	US-07-757-022B-92	US-07-757-022B-90	US-07-757-022B-88	US-09-579-181-1	US-07-757-022B-106	US-07-757-022B-118	US-07-757-022B-102	US-07-757-022B-114	US-09-579-181-2	US-09-919-172-98	US-09-976-594-22
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207	220	231	188	209	208	204	192	172	3118	156	156	157	157	2972	3256	3256
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1143	970.7	926	918.7	908.7	903.7	892.1	885.7	875.9	872.6	871	871	869	869	862.9	860.1	860.1
28	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: Gener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Turner, Katherine
APPLICANT: Turner, Katherine
APPLICANT: Howick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
TUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 19-104-19-91
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/390,901
FILING DATE: 29-DEC-1989
ATPORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08-AUG-1989
ATPORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08-AUG-1989
ATPORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 01-1989
ATPORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 01-1989
ATPORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 01-109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEPAX: (617)876-1170
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                                   Sequence 40, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
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                                                                PTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMD
                                                                                       PISRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVEMPEVTPDMD
                                                                                                                                                          YLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPAR
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APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SECUENCES: 143
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Vers

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/757,022B

FILING DATE: 19910910

CLASSIFICATION DATA:

APPLICATION NUMBER: US 07/643,502

FILING APPLICATION DATA:

APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-JUN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-DC-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/457,196

FILING DATE: 29-DC-1989

RIGH BATCH AND NUMBER: US 07/457,196

FILING DATE: 08-AUG-1989

ATTORNEY AGENT INFORMATION:

NUMBER: US 07/390,901
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87 CambridgePark Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI :
TELECOMMINICATION:
TELEPHONE: (617)876-1170
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CITY: Cambridge
STATE: Massachusetts
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                                                                                              Length 1361;
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100.0%; Pred. No. 2e-199;
tive 0; Mismatches 0;
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                         MOLECULE TYPE: protein US-07-757-022B-40
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Best Local Similarity
Matches 1361; Conserv
         TOPOLOGY:
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                                                                                           99.8%; Score 7308.7; DB 4; Length 1404; llarity 96.9%; Pred. No. 5.4e-199; Conservative 0; Mismatches 0; Indels 43;
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TELEFAX: (617)876-5851
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                            MOLECULE TYPE: protein
                                                                                         Query Match
Best Local Similarity
Matches 1361; Conserv
                                                                ; MOLECULE TY1
US-07-757-022B-2
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APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewinck, Rodney M.
TITLE OF INTENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS: #1.25 SOFTWARE: Patentin Release #1.0, Version 1404 CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196 1338 PSRTARAITTRSGQTLSKVWYNCP 1361 Inc APPLICATION NUMBER: US/07/757,022B FILING DATE: 19910910 APPLICATION NUMBER: US 07/457,196 FILING DATE: 29-DEC-1989 ; Sequence 62, Application US/07757022B ; Patent No. 6433142 ; GENERAL INFORMATION: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive CITY: Cambridge STATE: Massachusetts

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1080 1097 1140 1157 1200 1217

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61 KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP 120
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                             KPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPT
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99.8%; Score 7308.7; DB 4;
Best Local Similarity 96.9%; Pred. No. 5.4e-199;
Matches 1361; Conservative 0; Mismatches 0;
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TITLE OF INVENTION: TRIBONECTINS
FILE REPERENCE: 21486-026
CURRENT APPLICATION NUMBER: US/09/298,970A
CURRENT FILING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1404
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ORGANISM: Homo sapiens
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            ATTORNEY NUMBER: US 07/390,901
PILING DATE: 08-AUG-1989
ATTORNEY AGENT INFORMATION:
NAME: CSETY LUARN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELECHOME: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 amino acids
TYPE: AMINO ACID
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Conservative (
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PRIOR APPLICATION DATA:
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Best Local Similarity
Matches 1361; Conserv
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US-07-757-022B-62
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Sequence 48, Application US/07757022B Patent No. 6433142
GENERAL INFORMATION: APPLICANT: Genner, Thomas G. APPLICANT: Clark, Stephen C. APPLICANT: Turner, Katherine

US-07-757-022B-48

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 SGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAWKTLPIYLLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF
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                    Stimulating Factors
                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/646,114
FILING DATE: 20-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 20-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 20-DEC-1989
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 20-DEC-1989
ATTORNEY AGENT INFORMATION:
NUMBE: CSETT: LIAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5190
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
                                                                                 B. Genetics Institute,
87 CambridgePark Drive
                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
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REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: G:
TELECOMMUNICATION INFORMATION
TELEPHONE: (617)876-1170
TELEPAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1354 amino acids TYPE: AMINO ACID
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                                                                                                       STREET: 87 CambridgePa
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 97.0
Matches 1320; Conservative
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                                                                                     ADDRESSEE:
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Stimulating Factors

Megakaryocyte

Inc

Massachusetts

U.S.A.

02140

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OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-07M-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY, AGENT INFORMATION:
                                                                                                                                          ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
CITY: Cambridge
          GENERAL INFORMATION:
APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocy
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute
                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19
CLASSIFICATION:
Patent No. 6433142
                                                                                                                                                                        CITY: Can
STATE: Ma
COUNTRY:
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                                 PAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTT
                                                                                        TPBELAPTTPEEPTPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKE
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        PAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTTPT
                                                                    PKEPAPITKEPAPITPKEPAPIAPKKPAPITPKEPAPITPKEPAPITIKEPSPTTPKEPA
                                                                                                                                   PTTTKSAPTTTKBPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKE
                                                                                                                                                      PITIKSAPITIKEPAPITIKSAPITIPKEPSPITIKEPAPITPKEPAPITPKKPAPITPKK
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5190

1320 amino acids

AMINO ACID

1; 120 180 139 240 199 VETKETTTTINKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPA 300 09 79 -----ELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP 80 PPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEVKDNKKNRTKKKPTPKPPVVDEAG 61 KRVCTABLSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP PPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEVKDNKKNRTKKKPTPKPPVVDEAG SGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKFTSLTVNKETT 1 MAWKTLPIYLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF Gaps Ouery Match

96.4%; Score 7058.9; DB 4; Length 1320;
Best Local Similarity 97.0%; Pred. No. 5.8e-192;
Matches 1320; Conservative 0; Mismatches 0; Indels 41; MAWKTLPIYLLLLSVFVIQOVSSO------MOLECULE TYPE: protein US-07-757-022B-46 56 121 181 241

a à

; Sequence 46, Application US/07757022B

RESULT 7 US-07-757-022B-46

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US-07-757-022B-60
                                RESULT 8
US-07-757-022B-60
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Pred. No. 5.8e-192;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHWARE STEERING RELEASE #1.0, Vers CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION 530
PRIOR APPLICATION DATE: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 08-NUG-1989
APPLICATION NUMBER: US 07/457,196
FILING DATE: 08-NUG-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: US 07/390,901
FILING DATE: US 07/390,901
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Sequence 60, Application US/07757022B Patent No. 6433142 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                         E: Genetics Institute,
87 CambridgePark Drive
                                                                        APPLICANT: Gesner, Thomas G. APPLICANT: Clark, Stephen C. APPLICANT: Turner, Katherine APPLICANT: Hewick, Rodney M. TITLE OF INVENTION: Megakaryoc, NUMBER OF SEQUENCES: 143
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
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97.08;
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Best Local Similarity 97.03
Matches 1320; Conservative
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STATE: Massachusetts
COUMTRY: U.S.A.
ZIP: 02140
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SEQUENCE CHARACTERISTICS:
LENGTH: 1320 amino aci
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MOLECULE TYPE: protein
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                                        GYDYYAFSKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP
                                                                      GYDYYAFSKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 7049; DB 4;
Pred. No. 1.1e-191;
0; Mismatches 0;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/100 PATE:
APPLICATION NUMBER: US 07/100 PATE:
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FILING DATE: 18-JAN-1991
RALOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
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                                                                                                                           US-07-757-022B-42

Sequence 42, Application US/07757022B
Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: Gener, Thomas G.
                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                      APPLICANT: Geener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocy,
NUMBER OF SEQUENCES: 143
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
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ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 96.3
Matches 1311; Conservative
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COUNTRY: U.S.A.
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Gener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Clark, Stephen C.
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
INUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: CambridgePark Drive
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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APPLICATION NUMBER: US/07/757,022B FILNG APPLICATION S30 PRIOR APPLICATION NUMBER: US 07/643,502 FILNG APPLICATION NUMBER: US 07/643,502 FILNG APPLICATION NUMBER: US 07/546,114 FILNG APPLICATION NUMBER: US 07/546,114 FILNG APPLICATION NUMBER: US 07/546,114 FILNG APPLICATION NUMBER: US 07/457,196 FILNG APPLICATION NUMBER: US 07/457,196 FILNG APPLICATION NUMBER: US 07/457,196 FILNG APPLICATION NUMBER: US 07/457,196 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPLICATION NUMBER: US 07/390,901 FILNG APPL
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Pred. No. 1.5e-191;
0; Mismatches 0;
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REGISTRATION NUMBER: 31,822
REPERSONCYDOCKET NUMBER: GI ST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1363 amino aci
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                   PPSGASQTIKSTTKRSPKPPNKKKTKKV1ESEEITEVKDNKKNRTKKKPTPKPPVVDEAG
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	978 POKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMISTMPELNPTSRIABAMLQITTRPN 1037	ò
Qy 301 LITPKEPTPITE	-⊢	qa
	918 ISTITQDITPFKITILKITILAPKVITITKKIITITEIMNKPEETAKPKDRATNSKATIPK 977	ò
Qy 241 VETKETTTTNK	-⊢	qq
Db 140 SGLDNGDFKVTJ	858 IKTPAATKPEMITTAKDKTTBEDLKTTPETTTAAPKMIKETATTTEKTTESKITATTQV 917	δ
Qy 181 SGLDNGDFKVT	800 KPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPT 859	qq
	798 KPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPT 857	οy
Qy 121 PPSGASQTIK	740 TAPITLKEPAPITPKKPAPKELAPITIKGPISITSDKPAPITPKETAPITPKEPAPITPK 799	qq
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Qy 61 KRVCTAELSCKC		QQ
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Best Local Similarity Matches 1317; Conservat	618 PEEPAPITPKAAAPNIPKEPAPITPKEPAPITPKEPAPITPKETAPITPKGTAPITIKEP 677	à
Query Match	560 APTAPKEPAPTTPKETAPTTPKKLTPTTPBKLAPTTPEKPAPTTPEBLAPTTPEEPTPT 619	qq
; ORGANISM: Homo sapien: US-10-164-595-58		δ
	TTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTTKKP	qq
SOFTWARE: Patentin veri	ТТКЅАРТТРКЕРЅРТТКЕРАРТРАРТРАРТРАРТРАТОВ В СТ. 25.	ò
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; GENERAL INFORMATION: ; APPLICANT: OxiGene Te: ; TITLE OF INVENTION: R	378 APTITKSAPITPKEPAPITPKEPAPITPKEPAPITPKEPTPTPKEPAPITKEPAPITPK 437 	Sy Dp
Sequence 58, Application Patent No. 6657054		qq
RESULT 11 IR-10-164-595-58	318 TIPKEPIPITIKSAPITPKEPAPITIKSAPITPKEPAPITTKEPAPITPKEPAPITTKEP 377	δλ
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Qy 1338 PSRTARALTTR		70
Db 1280 SPARLAYODKG	TOHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDG 2	qq
Oy 1278 SPARLAYODKG	TQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDG 25	à
Db 1220 FFKRGGSIQQY		qq
Oy 1218 FFKRGGSIQOY	VKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDT	Qy
Db 1160 RCNCEGKTFFF	EHSVSENQESSSSSSSSTIW 13	ΩP
Qy 1158 RCNCEGKTFFF	PPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITE	ò
Db 1100 DETNICNGKPV	ELSCKGRCFESFERGEECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP 79	දු අ
QY 1098 DETNICUGKPV	KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTS!	à

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egulated Angiogenesis Genes and Polypeptides
3 Rl
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2002-06-10
                                                                                                                                                                                                                                                          RSGQTLSKVWYNCP 1361
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                                                                                                                                                                                                                 Version #1.25
                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
                                Inc.
                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
                                                                                                                                                                                                                                                  UMBER: US/07/757,022B
19910910
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
           CORRESPONDENCE ADDRESS:
ADDRESSEB: Genetics Institute,
STREET: 87 cambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: CSET, LUANN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1314 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                           02140
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Matches 1281;
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; Sequence 50, Application US/07757022B
; Patent No. 6433142
; Patent INFORMATION:
    APPLICANT: Gesner, Thomas G.
    APPLICANT: Clark, Stephen C.
    APPLICANT: Turner, Katherine
    APPLICANT: Hewick, Rodney M.
    TITLE OF INVENTION: Megakaryocyte Stimulating Factors
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Inc

3: Genetics Institute, 87 CambridgePark Drive

U.S.A. 02140

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APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.3
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 18-7AN-1931
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 08-AUG-1989
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION: TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617)876-117
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                               STREET: 87 Cambridge
CITY: Cambridge
STATE: Massachusetts
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MEDIUM TYPE: Floppy
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: 1313 amino acids AMINO ACID

7 180 132 240 192 241 VETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPA 300 252 79 80 SSSSSSTIWKIKSSKNSAANRELQKKL-----KVKDNKKNRTKKKPTPKPPVVDEAG 61 KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP 121 PPSGASQTIKSTIKRSPKPPNKKKTKKVIESEEITEVKDNKKNRIKKKPTPKPPVVDEAG 193 VETKETTTTNKÇISTDGKEKTTSAKETÇSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPA 1 MAWKTIPIYLLILISVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF -----BLSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEEHSVSENQESSSSS SGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETT Gaps DB 4; Length 1313; 48; 26; Indels 93.1%; Score 6820.2; DB 4.94.0%; Pred. No. 3.3e-185; ive 8; Mismatches 26; 1 MAWKTLPIYLLLLSVFVIQOVSSQ-Query Match
Best Local Similarity 94.0°
Matches 1279; Conservative 56 181 g $\overset{\circ}{\circ}$ Db

RESULT 13 US-07-757-022B-142

Sequence 142, Application US/07757022B Patent No. 6433142

GENERAL INFORMATION:

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U.S.A.
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RESULT 14
US-07-757-022B-44
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                                                                   313 PAPITIPKEPAPITITKEPAPITITKSAPITIPKEPAPITIPKKPAPITIPKEPAPITIPKEPIPIT
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             361 PAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTPTT
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2 180 149 120 89 9 25 90 SGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETT 181 SGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETT 61 KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP 121 PPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEVKDNKKNRTKKKPTPKPPVVDEAG 1 MAWKTLPIYLLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF Gaps Score 6784.9; DB 4; Length 1270; Pred. No. 3.1e-184; 0; Mismatches 0; Indels 91; Sequence 44, Application US/07757022B

Sequence 44, Application US/07757022B

Sequence 44, Application US/07757022B

Sequence 44, Application US/07757022B

Sequence 44, Application US/07757022B

SEPPLICANT: Clark, Stephen C.

APPLICANT: Turner, Katherine
APPLICANT: Turner, Katherine
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.

TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc. ----ELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCA--1 MAWKTLPIYLLLLSVFVIOQVSSQ-------ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: CLASSIFICATION: 530
CLASSIFICATION DATA:
APPLICATION UNBER: US 07/643,502
FILING DATE: 18-0AN-1991
PRIOR APPLICATION UNBER: US 07/546,114
APPLICATION UNBER: US 07/546,114
FILING DATE: 29-UNN-1990
PRIOR APPLICATION UNBER: US 07/457,196
FILING DATE: 29-DEC-1889
PRIOR APPLICATION UNBER: US 07/457,196
FILING DATE: 29-DEC-1889
FILING DATE: 08-AUG-1889
FILING DATE: 08-AUG-1988
ATTORNEY AGENT INFORMATION: APPLICATION NUMBER: US/07/757,022B FILING DATE: 19910910 5190 NAME: Cserr, Luann REGISTRATION NUMBER: 31,822 REFERENCE/DOCKET NUMBER: GI TELECOMMUNICATION INFORMATION: INFORMATION FOR SEQ ID NO: 44.
SEQUENCE CHARACTERISTICS:
LENGTH: 1270 amino acids Query Match 92.7%; Best Local Similarity 93.3%; Matches 1270; Conservative (617)876-1170 (617)876-5851 MOLECULE TYPE: protein STREET: 87 Cambridgel CITY: Cambridge STATE: Massachusetts TYPE: AMINO ACID TOPOLOGY: linear 셤

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KRVCTABLSCKGRCFESFERGRECDCDAQCKKYDKCCPDYSSFCAEVHNPTSPPSSKKAP 120
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80.1%; Score 5867.7; DB 4

Best Local Similarity 96.2%; Pred. No. 2.5e-158;

Matches 1097; Conservative 0; Mismatches 0;
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87 CambridgePark Drive
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REGISTRATION NUMBER: 31,822
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INFORMATION FOR SEQ ID NO: 104:
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TELECOMMUNICATION INFORMATION:
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AMINO ACID
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                                                                                                                                                                                                                                                                                   CITY: Cambridge
STATE: Massachusetts
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US-07-757-022B-104
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US-07-757-022B-104
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1321 GYDYYAFSKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP
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                                                                                                                                                                                                                                                     APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER REACABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-7AN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-7UN-1990
PRIOR APPLICATION DATA:
APPLICATION UNDERE: US 07/457,196
FILING DATE: 29-DEC-1889
PRIOR APPLICATION DATA:
APPLICATION UNDERE: US 07/390,901
FILING DATE: 08-AUG-1889
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                               ; Sequence 104, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
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Search completed: October 13, 2004, 11:59:22 Job time : 30.6582 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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October 13, 2004, 11:23:49; Search time 138.466 Seconds (without alignments) 3171.696 Million cell updates/sec Run on:

1 MAWKTLPIYLLLLSVFVIQ......ARAITTRSGQTLSKVWYNCP 1361 SEQ1-G 7323 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.1 Scoring table:

1356558 seqs, 322682953 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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; cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

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14: cgn2_6/ptodata/1/pubpaa/US10P_PUBCOMB.pep:*

15: cgn2_6/ptodata/1/pubpaa/US10P_PUBCOMB.pep:*

16: cgn2_6/ptodata/1/pubpaa/US10P_PUBCOMB.pep:*

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18: cgn2_6/ptodata/1/pubpaa/US10P_PUBCOMB.pep:*

19: cgn2_6/ptodata/1/pubpaa/US10P_PUBCOMB.pep:*

19: cgn2_6/ptodata/1/pubpaa/US10P_PUBCOMB.pep:* Published Applications AA:* 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	0, Appl	, Appl	, Appli	, Appli	2, Appl	48, Appl	6, Appl	0, Appl	2, Appl	2, Appl	0, Appl	42, App	4, Appl	104, App
Description	Sequence 40, App	Sequence 30, Appl	Sequence 1,	Sequence 2	Sequence 6	Sequence 4	Sequence 4	Sequence 6	Sequence 42,	Sequence 5	Sequence 5	Sequence 142,	Sequence 4	Sequence 1
ID	US-10-124-557-40	US-09-802-207-30	US-09-897-188-1	US-10-124-557-2	US-10-124-557-62	US-10-124-557-48	US-10-124-557-46	US-10-124-557-60	US-10-124-557-42	US-10-124-557-52	US-10-124-557-50		US-10-124-557-44	US-10-124-557-104
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% Query Match Length DB	1361	1404	1404	1404	1404	1354	1320	1320	1311	1363	1314	1313	1270	1140
% Query Match	100.0	8.66	8.66	8.66	8.66	96.7	96.4	96.4	96.3	96.2	93.4	93.1	92.7	80.1
Score	7323	7308.7	7308.7	7308.7	7308.7	7084.3	7058.9	7058.9	7049	7044.6	6836.3	6820.2	6784.9	5867.7
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ALIGNMENTS

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APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: FLORDY disk
COMPUTER: FLORDY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: CURROWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genetics Institute, Inc. STREET: 97 CambridgePark Drive CITY: Cambridge STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02140 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/643,502
                                            ; Sequence 40, Application US/10124557; Publication No. US20020137894A1; GENERAL INFORMATION:
                          US-10-124-557-40
RESULT 1
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APPLICANT: Carpten, John APPLICANT: Trent, Jeffrey
APPLICANT: Trent, Jeffrey
APPLICANT: Trent, Jeffrey
APPLICANT: Marcelino, Jose
TITLE OF INVENTION: Novel Methods and Reagents for the Treatment of Osteoarthritis
FILE REFERENCE: Case-06212
CURRENT APPLICATION NUMBER: US/09/802,207
CURRENT FILING DATE: 2001-08-29
PRIOR PILING DATE: 2000-07-19
PRIOR FILING DATE: 1999-07-23
NUMBER: 0145,328
RIOR FILING DATE: 1999-07-23
NUMBER: PARELICATION NUMBER: 60/145,328
RIOR FILING DATE: 1999-07-23
NUMBER: PARELICATION NUMBER: 60/145,328
PRIOR FILING DATE: 1999-07-23
NUMBER: PARELICATION NUMBER: 80/145,328
PRIOR FILING DATE: 1999-07-23
NUMBER: PARELICATION NUMBER: 80/145,328
PRIOR FILING DATE: 1999-07-23
NUMBER: PARELICATION NUMBER: 80/145,328
PRIOR FILING DATE: 1999-07-23
NUMBER: PARELICATION NUMBER: 80/145,328
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                                                                    PTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 30, Application US/09802207; Publication No. US2020086824A1; GENERAL INFORMATION: APPLICANT: Warman, Matthew
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100.0%; Pred. No. 1.7e-169;
ive 0; Mismatches 0; Indels 0;
                   NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
RESERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                       LENGTH: 1361 amino acids
                                                                                                                           TELEFAX: (617)876-5851
ATTORNEY/AGENT INFORMATION:
                                                                                                                                               INFORMATION FOR SEQ ID NO: 40: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                               TYPE: amino acid
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US20020137894A1
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Best Local Similarity 96.9
Matches 1361; Conservative
Publication No.
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RESULT 4 US-10-124-557-2 ; Sequence 2, Application US/10124557

1; 300 120 156 240 120 180 197 9 121 PPSGASQTIKGTTKRSPKPPNKKKTKKVIESEEITEEHSVSENQESSSSSSSSSTIW 1 MAWKTLPIYLLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF 1 MAWKTLPIYLLILISVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF 61 KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP ·VKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTST TOHNKVSTSPKITTAKPINPRPSLPPNSDISKETSLTVNKETTVETKETTTNKQTSTDG 241 IQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDG Gaps 99.8%; Score 7308.7; DB 13; Length 1404; 96.9%; Pred. No. 3.9e-169; cive 0; Mismatches 0; Indels 43; INVENTION: Megakaryocyte Stimulating Factors PPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITE PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-0AN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/45,196
FILING DATE: 29-EC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION: ZIP: 02140
COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive CITY: Cambridge TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-124-557-2 NAME: CBELT, LUANN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMUNICATION INFORMATION:
TELEPHONE: (617)876-1170 LENGTH: 1404 amino acids GENERAL INFORMATION: APPLICANT: Turner, Katherine Clark, Stephen C. Jacobs, Kenneth Hewick, Rodney M. Gesner, Thomas G. TELEFAX: (617)876-5851 STATE: Massachusetts COUNTRY: U.S.A. CHARACTERISTICS INFORMATION FOR SEQ ID NO: 2 NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS: à

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258 KEKITSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTFPKEPAS 317	Qy 1338 PSRTARAITTRSG
	Db 1381 PSRTARAITTRSG
318 TTPKEPTPITIKSAPTTPKEPAPTTIKSAPTTPKEPAPTTTKEPAPTTTKEPAPTTTKEP 377 	RESULT 5 US-10-124-557-62 ; Sequence 62, Application
378 APTITKSAPTIPKEPAPTIPKEPAPTIPKEPAPTIPKEPIPTIPKEPAPTIKEPAPTIFK 437 	; Publication No. US2002013 ; GENERAL INFORMATION: ; APPLICANT: Turner,
	Jacobs, Hewick, Genner, TITLE OF INVENTION
498 TTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKP 557 	S OF SPON ADDR
558 APTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPT 617 	; CITY: Cambrid ; STATE: Massacl ; COUNTRY: U.S.; ; ZIP: 02140
618 PEEPAPTTPKAAAPNTPKEBAPTTPKEBAPTTPKETAPTTPKGTAPTTLKEP 677 	COMPUTER READABLE 1 HEDIUM TYPE: COMPUTER: 1BM COMPUTER: 1
678 APTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKG 737 	SOFTWARE: Pate CURRENT APPLICATION PAPLICATION IN
738 TAPTTLKEBAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPK 797 	CLASSIFICATION PRIOR APPLICATION PELLING DATE:
798 KPAPTTPETPPTTSEVSTPTTIKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPT 857 	APPLICATION NI FILING DATE: 2 APPLICATION NI FILING DATE: 7 FILING DATE: 7
858 IKTPAATKPEMITTAKDKTTERDLRITTAAPKMTKETATTTEKTTESKITATTOV 917 	; APPLICATION NO ; FILING DATE: (; ATTORNEY/AGENT INFO ; NAME: CEEPT I
918 TSTTODTTPFKITTLKTTTLAPKVTTTKKTITTTBIMNKPEBTAKPKDRATNSKATTPK 977 	REGISTRATION REFERENCE/DOCK TELECOMMUNICATION 1 TELECHONE: (4)
978 POKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMISTMPELNPTSRIAEAMLQTTTRPN 1037 	WHHC
1038 QTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDXLPRVPNQGIIINPMLS 1097 	; TYPE: amino ac ; TOPOLOGY: line ; MOLECULE TYPE: prot ; SEQUENCE DESCRIPTION
1098 DETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFT 1157 	557-62 tch
1158 RCNCEGKTFFFKDSQYMRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKOWPESVY 1217 	S 1361; Conservat 1 MAWKTLPIYLLL
1218 FFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRFEBRAIGPSQTHTIRIQY 1277 	Db 1 MAWKTLPIYLLILL Qy 61 KRVCTAELSCKGRC
1278 SPARLAYODKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYYAFSKDQYYNIDV 1337 	Db 61 KRVCTABLSCKGRC Qy 121 PPSGASQTIKSTTK

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CCESFERGRECDCDAQCKKYDKCCDDYESFCAEVHNPTSPPSSKKAP 120
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96.9%; Pred. No. 3.9e-169;
ve 0; Mismatches 0; Indels 43; Gaps
                                                                                                                                                       ier, Katherine
k, Stephen C.
Dbs, Kenneth
ck, Rodney M.
er, Thomas G.
NOTES: 143
ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                              PE: Floppy disk

IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
MION DATA:
NUMBER: US/10/124,557
PE: 16-Apr-2002
ATION: AURIONA.
AUMBER: US 07/643,502
NN NUMBER: US 07/643,502
PE: 18-AAN-1991
NN NUMBER: US 07/546,114
PE: 29-AUN-1990
NN NUMBER: US 07/546,114
PE: 29-DEC-1989
NN NUMBER: US 07/457,196
PE: 29-DEC-1989
NN NUMBER: US 07/457,196
PE: 29-AUG-1989
NN NUMBER: US 07/457,196
PE: 29-AUG-1989
PE: 08-AUG-1989
PE: US 07/457,196
PE: US 07/457,196
PE: US 07/457,196
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N UVURBER: 31,822
OCKET NUMBER: GI 5190
N INFORMATION:
(617)876-1170
IT)876-5851
D NO: 62:
ERISTICS:
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ION: SEQ ID NO: 62:
GQTLSKVWYNCP 1361
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1;
SCAGRCGEGYSRDATCNCDYNCQHYMECCPDF 60
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tches 26; Indels 7; Gaps
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..0, Version #1.25
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QY 1141 RITEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQI 1200	RESULT 7 19-124-557-46 19-10-124-557-46	Query Match 96.4%; Score 7058.9; DB 13; Length 1320; Best Local Similarity 97.0%; Pred. No. 4.1e-163; Matches 1320; Conservative 0; Mismatches 0; Indels 41; Gaps 1;
61 KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP 120 61 KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP 120 61 KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEGHSVSENQESSSS 120 121 PPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEVKDNKKNRTKKKPTPKPPVVDEAG 180 121 SSSSSSTIWKIKSSKNSAANRELQKKLKVKDNKKNRTKKKPTPKPPVVDEAG 173 181 SGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETT 240 174 SGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETT 233 241 VETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPPSKVLAKPPKAETTTKGPA 300 234 VETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPPSKVLAKPPKAETTTKGPA 293	101 ILTPREPRITIVEBAPTTYREAPPTTYREAPPTTYREAPPTTYREAPTTYREAPTTYRE 35 361 PAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRESPECTOR 364 PAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 35 365 PAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREBAPTYREBEPTY 4.0 364 PAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREBEPTYREBEPTY 4.1 4.14 PKREATTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREBEPTYREBEPTYRE 54 4.15 PKREATTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREBEPTYREBEPTYRE 54 4.16 PKREATTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREBEPTYREBEPTYRE 54 4.16 PKREATTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREBEPTYRE 54 4.17 PKREATTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREBEPTYRE 56 5.18 PAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREBEPTYRE 56 5.19 PTREATTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 56 5.10 PAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 56 5.10 PAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 56 5.10 PAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 57 5.11 PAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 57 5.12 PAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 57 5.13 PAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 57 5.14 PAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 57 5.15 PAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 57 5.16 TAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 57 5.17 KETAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 57 5.18 PAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 57 5.19 TAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 57 5.10 PTREATTYREAPTTYREAPTTYREAPTTYREAPTTYRE 57 5.11 PAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 57 5.12 PAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 57 5.13 PATTYREAPTTYREAPTTYREAPTTYREAPTTYRE 57 5.14 PAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 57 5.15 PAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 57 5.16 TAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 57 5.17 KETAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 57 5.18 TAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 57 5.19 TTREATTERNETTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYREAPTTYRE 57 5.10 TTREATTERNETTYREAP	1074 YLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPAR 1133

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QY	RESULT 8 US-10-124-557-60 ; Sequence 60, Application US/10124557 ; Publication No. US20020137894A1 ; GENERAL INFORMATION:	NUMBER OF SEQUENCES: 143 CORESPONDENCES: 143 ADDRESSER: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge STRYE: Massachusetts COUNTRY: U.S.A. ZIP: 02140 MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible COMPUTER: IDM PC Compatible COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible COMPUTER: Delease #1 O Version #1.25	124,557 643,502 546,114 457,196 390,901	ATTORNEY/AGENT INFORMATION: REALSTRATION NUMBER: 31,822 REALSTRATION NUMBER: 31,822 REPERBOOKET UNBER: G1 5190 TELECOMMUNICATION INFORMATION: TELEPROME: (61)876-1170 TELEPROME: (61)876-1170 TELEPROME: (61)876-1551 INFORMATION FOR SEQ ID NO: 60: SEQUENCE CHARACTERISTICS: TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: Dratein SEQUENCE DESCRIPTION: SEQ ID NO: 60: US-10-124-557-60
1 MAWKTLDIYLLLLSVPVIQQVSSQDLSSCAGRCGBGYSRDATCNCDYNCQHYMECCPDF 60	101 LITPKEPTPTTPKEPASTTPKEPTPTTKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKE 260 LITPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKE 361 PAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTTKSAPTTTKEPAPTTTKE 320 PAPTTPKEPAPTTTKSAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTTKSAPTTTKSAPTTTKEPAPTTAFKEPAPTT	481 PTTTKSAPTTTK 440 PTTTKSAPTTTK 541 PAPTTPKEPAPT 500 PAPTTPKEPAPT 601 TPBELAPTTPEE 560 TPBELAPTTPEE	661 TAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPK [841 PTPKALENSPKEPOPTTKTPAATKEEMTTTAKOKTTERDLATTTAARTKETAT 900 800 PTPKALENSPKEPOPTTKTPAATKEEMTTTTAKOKTTERDLATTTAARTKETAT 900 801 TTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMKKPEB 960 860 TTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMKKPEB 910 961 TAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTTTPIMKKPEB 919 962 TAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELN 979 1021 PTSRIABAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAGGETPHMLLRPHVFMPEVTPDMD 1080
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                                                                                                                                    1160 VAALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRRR
                                                                                                                   RITEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQI
                                                                                                                                                                             VAALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRR
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|GYDYYAFSKDQYYNIDVPSRTARAITTRSGGTLSKVWYNCP 1320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stimulating
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 22-DEC-1989
APPLICATION NUMBER: US 07/457,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEMS: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-10-124-557-42
Sequence 42, Application US/10124557
Fublication No. US20020137894A1
SENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kennern
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Sti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genetics Insti
STREET: 87 CambridgePark
CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1311 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                        VETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPA
                                                              1 MAWKTLPIYLLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF
                                                                                                                                                    ----ELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP
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                                          Gaps
          DB 13; Length 1320,
                                        41;
                                       Indels
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                                                                                         MAWKTLPIYLLLLSVFVIQQVSSQ------
         Score 7058.9;
Pred. No. 4.16
                                     0; Mismatches
   Query Match
Best Local Similarity 97.0%;
Matches 1320; Conservative
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                                                             PTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMD
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APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION - CURNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-APN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/490,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
CONNTRY: U.S.A.
ZID: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PACHOLIN ROLESSE SOFTWARE: PACHOLIN Release #1.0, v
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Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte St
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
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STREET: 87 CambridgePark Drive
CITY: Cambridge
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFRAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 52, Application US/10124557 Publication No. US20020137894A1 GENERAL INFORMATION:
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                                                                                                                     Gaps
                                                                                                                   50;
                                                                                       Length 1311;
                                                                                                                     Indels
                                                                     Score 7049; DB 13;
Pred. No. 7e-163;
                                         42:
    TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-124-557-42
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                                                                                       96.3%;
96.3%;
                                                                                                                     Conservative
                                                                                                      Best Local Similarity
Matches 1311; Conserv
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OF INVENTION: Megakaryocyte Stimulating Factors OF SEQUENCES: 143
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/490,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
WIEDLIW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute,
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                           PSRTARAITTRSGQTLSKVWYNCP 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 50, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: <Unknown>
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Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
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Pred. No. 9.4e-163;
0; Mismatches 0; Indels 84;
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                                                                     52
                               TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                          INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1363 amino acids
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Best Local Similarity 94.0
Matches 1320; Conservative
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SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002

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KETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAE
                                                                                 PTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKWTKETAT
                                                                                                                                              PTSRIAEAMLOTTTRENQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMD
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                                                                                                                           TTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEE
                                                               PTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GYDYYAFSKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAV-1991
APPLICATION NUMBER: US 07/546,114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 142, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
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COMPUTER READABLE FORM:
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Pred. No. 1e-157;
8; Mismatches 25; In
                                                                         5190
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                                          NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
RESERRENCE/DOCKET NUMBER: GI 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-1170
TELEPAK: (617)876-5851
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 NO.
                                                                                                                                                                   LENGTH: 1314 amino acids
TYPE: amino acid
                                                                                                                                                                                               TOPOLOGY: linear
NOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
US-10-124-557-50
              FILING DATE: 08-AUG-19 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 94.1%;
Matches 1281; Conservative
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Clark, Stephen C.
Clark, Stephen C.
Hawick, Rodiney M.
Genneth,
Hewick, Rodiney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GYDYYAFSKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP 1361
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                      EPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTT
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
RPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <unversely compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the
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STREET: 87 CambridgePark Drive
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US-10-124-557-44

Sequence 44, Application US/10124557

Publication No. US20020137894A1

GENERAL INFORMATION:
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COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.1%; Score 6820.2; DB 13; Length 1313;
llarity 94.0%; Pred. No. 2.5e-157;
Conservative 8; Mismatches 26; Indels 48;
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 142:
                                                                                                                         REGISTRATION NUMBER: 31,822
REGISTRATION NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAWKTLPIYLLLLSVFVIQQVSSQ-
                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-8851
INFORMATION FOR SEQ ID NO: 142:
                                                                                                                                                                                                                                                                                                               LENGTH: 1313 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 1279; Conserv
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TAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPK
                  EPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTP
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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US-10-124-557-104
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                                                                                                                                                                                                                                                                                                                                                                                      Score 6784.9; DB 13; Length 1270;
Pred. No. 1.7e-156;
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          OR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
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                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAWKTLPIYLLLLSVFVIQQVSSQ-
                                                                                                                                                                                                                     TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1270 amino acids
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ilarity 93.3%;
Conservative (
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Best Local Similarity
Matches 1270; Conserv
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                      PEEPAPTTPKAAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEP
                                                                                        PEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEP
                                                                                                                                              APTIPKKPAPKELAPITIKEPISTISDKPAPITIPKGTAPITPKEPAPITPKEPAPITIPKE
    APTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 74, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: «Unknown»

OR APPLICATION DATA:
APPLICATION UNMER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/457,196
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
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US-10-124-557-74
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                                                                                                                                                                                                                                                                                                                                                                                                                                         80.1%; Score 5867.7; DB 13; Length 1140; 96.2%; Pred. No. 2.6e-134; ive 0; Mismatches 0; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITE------
                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-7M-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY_AGENT INFORMATION:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                          5190
                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
                                                                                                                                                                                                     NAME: CSETT, LUADN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                LENGTH: 1140 amino acids
                                                                                                                                                                                                                                                                                   TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity 96.2
Matches 1097; Conservative
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Search completed: October 13, 2004, 11:53:23 Job time : 146.466 secs
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                                                                                                                                                                                                                                                              61 KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP
                                                                                                                                                                                                                                                                                                                            -----EVKDNKKNRTKKKPTPKPPVVDEAG
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                                                                                                                                                                                                                   1 MAWKILPIYLLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF
                                                                                                                                                                         Score 5485.7; DB 13; Length 1038;
Pred. No. 4.2e-125;
0; Mismatches 0; Indels 323;
                                                                                                                                                                                                                                                                            -----BLSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCA
                                        5190
                                                                                                                                               74:
                  NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 51
TELECOMMUNICATION INFORMATION:
TELECHONE: (617)876-1170
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-1170
TELEPHONE: GIPN 876-1170
TELEPHONE: GARACTERISTICS:
LENGTH: 1038 amino acids
                                                                                                           TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-124-557-74
                                                                                                                                                                                                                                   1 MAWKTLPIYLLLLSVFVIQQVSSQ-
FILING DATE: 08-AUG-19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                               74.9%;
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Best Local Similarity 76.39
Matches 1038; Conservative
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

October 13, 2004, 11:23:49; Search time 149.642 Seconds (without alignments) 5233.063 Million cell updates/sec Run on:

SEQ1-G 73.23 1 MAWKTLPIYLLLLLSVFVIQ.....ARAITTRSGQTLSKVWYNCP 1361 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.1

Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	092954	09BX49	O6ZMZ5	BAD18580	99MD99	077765	MUC2 HUMAN	Q9VR49	Q7KTF6	AAS64673	Q6DNC4	Q7 PMD5	O6SSE6	AAS07044	O6SSE8	AAS07042	Q6QJF3	AAS83977	SLP1 CLOTM	MUSB_HUMAN	Q7KTP5	AAN10531	Q8IR51	Q8IR52	081018	AAN10358	076894	Q8WWQ4	09N4S7	Q8WZ42	Q9VPG1
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٠	Query Match	99.8	99.6	63.3	63.3		\sim		18.9		18.3	18.2	17.9	17.2	17.2	16.2	16.2	16.2	16.2	16.1	15.6	15.5	15.5	15.3	15.3	15.3	15.3	•	15.2	15.1	٠.	•
	Score	7308.7		4634.6	634	3995.3	714	413	381	1339.8	1339.8	1333	1310.1	1256.8	1256.8	1184.8	1184.8	1183	1183	1179	1139.6	1137.8	1137.8	1121.9	1121.8	1118.3	1118.3	11	1115.4	1108.3	1096.9	1080.9
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Q10465 homo sapien P70670 mus musculu Q8h6q5 phytophthor	Aap74661 phytophth Q7qkk7 anopheles g O96449 phytophthor O9w223 drosophila	, 0 .0 0	Q81sf7 caenorhabdi Q20007 caenorhabdi Q9vc00 drosophila Q757n5 ashbya goss
Q10465 P70670 Q8H6Q5	AAF74661 Q7QKK7 O96449 O9W2Z3	Q8ISF5 Q9LIE8 Q8ISF6	Q81SF7 Q20007 Q9VC00 Q757NS
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ALIGNMENTS

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                                                                                                                                                                                                                                           1 MAWKILPIYLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPPF
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                                            QTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLS
                                                                                                                            DEINICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPBRPRBPRRITEVWGIPSPIDTVFT
                                                                                                                                                                                                                                                                                    SPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYYAFSKDQYYNIDV
                                                                                                       DETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFT
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InterPro; INTOUGH, 120.
InterPro; INTOUGHE; Somatomedin_B.
Fam; PR00045; Hemopexin; 2.
Fam; PR00022; SOMATOMEDINB; 2.
PRINTS; PR00022; SOMATOMEDINB; 2.
SMART; SM00120; HX; 2.
SMART; SM0012, SO; 2.
PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
PROSITE; PS0024; SOMATOMEDIN B; 2.
SEQUENCE 1404 AA; 151076 MW; 782AL1746B3FDEES CRC64;
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL133553; CAC36090.1; --
HSSP; P04004; 10C0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JMA-2004 (TrEMBLrel. 26, Last annotation update)
BG174L6.2 (MSF: megakaryocyte stimulating factor ).
Name=bG174L6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.6%; Score 7293.7; DB 2;
llarity 96.7%; Pred. No. 1.1e-142;
Conservative 0; Mismatches 3;
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Matches 1358; Conserv
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                                                                  1 MAWKTLPIYLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF
                                                                                       MAWKTLPIYLLLLSVFVIQQVSSQDLSSCAGRGGEGYSRDATCNCDYNCQHYMECCPDF
                                                                                                                              KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP
                                        Gaps
         Length 1404;
                                        43;
                                      Indels
            DB 2;
       Score 7308.7; DB 2;
Pred. No. 5.6e-143;
0; Mismatches 0;
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          Query Match
Best Local Similarity 96.9%;
Matches 1361; Conservative
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SSKNSAP NKVSTSE NKVSTSE TTSAKET	13-61 TIPKEEPPTTIKEAPTTPKERPAPTTPKEAPATTTKEPAPTTTKEPATTTKEPAPTTTKEPAPTTTKEPATTTKEPAPTTTKEPAPTTTKEPATTTKEPAPTTTKEPATTTKEPATTTKEPATTTKEPATTTKEPATTTKEPATTTKEPATTTKEPATTTKEPATTTKEPATTTKEPATTTKEPATTTKEPATTTEKTTTEK	1201 RCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVY 1260

Db 910 PSRTARAITTRSGQTLSKVWYNCP 933	RESULT 4 BAD18580 ID BAD18580 PRELIMINARY; PRT; 933 AA.	BAD18580; 12-MAY-2004 (TrEMBLrel. 27, Created) 12-MAY-2004 (TrEMBLrel. 27, Last sequence update) 12-MAY-2004 (TrEMBLrel. 27, Last annotation update)	CDNA FLJ16561 fis, clone SYNOV400 sapiens proteoglycan 4, (megakary superficial zone protein, campton pericarditis syndrome) (PRG4).		RN [1] RP SEQUENCE FROM N.A. RC TISSUES, TISSUE, RA OLA I., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T., RA Ota I., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T.,	Irie R., Otsuki T., Sato H., Wakamatsu A., Isuit S., Isumamood Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., F Barasteuma M. Mirakawa K., Kanehori K., Takahashi-Fujii A., Os		DR EMBL; AK131434; BAD18580.1; SQ SEQUENCE 933 AA; 102512 MW; B883773C5BC21A23 CRC64;	Query Match 63.3%; Score 4634.6; DB 2; Length 933; Best Local Similarity 63.3%; Pred. No. 6.56-88; Matches 889; Conservative 0; Mismatches 1; Indels 514; Gaps 3;	1 MAWKTLPIYLLLLLSVPVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCOHYMECCPDF 6	CDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP	Db 26 ELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP 79 Qy 121 PPSGASOTIKSTTKRSPKPPKKKKYKVIESEEITE	Db 80 PPSGASQTIKSTTKRSPKPPNKKTKKVIESEEITEEHSVSENQESSSSSSSSSSSSTIR 139	140	200		CY 318 TIPKEPTPITIKSAPITPKEPAPITITKSAPITPKEPAPITIKEPAPITIKEP 377	378 APITIKSAPITPKEPAPITPKKPAPITPKEPAPITPKEPAPITPKBPAPITKEPAPITE	Db 371 370 Qy 438 EPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPT 497	Db 371 370
			371	TTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTFKKP	3/153 APTAPKEPAPTTPKETAPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPT 617	PEEPAPTIPKAAAPNTPKEPAPTIPKEPAPTIPKEPAPTIPKETAPTIPKGTAPTILKEP	APTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKG	371 370 738 TAPTILKEPAPTIPKKPAPKELAPTITKGPISTTSDKPAPTIPKETAPTTPKEPAPTIPK 797	, ;	GVPT	858 TKTPAATKPEMTTTAKDKTTBRDLRTTPETTTAAPKWTKETATTTEKTTESKITATTTQV 917 	FF-	· ц—	POKPTKAPKKPISTKKPKTMPRVRKPKITPIPKKMISIGNELDNISKILBAATLUITEN QTPNSKLUEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLS	IDTVFT	670 DETNICHGERPUGGLTTLRNGTLVAFRGHYFWMLSPESPEARRITEVMGIPSPLDTVFT 729 1158 RCNCEGKTFFFKDSOYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKXKNWPESVY 1217	O RCNCEGKIFFFKDSQYWRFINDIKDAGYFKPIFKGFGGLTGQIVAALSTAKYKN	1218 FFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMIQVRKKKEFKALGFSQIBLIKLY 		

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                                                                                      human
                                                                                                                                                                                                                                                                                                                        Length 1054;
                                                                                       | Transcript, Contraction, and Mapping of the Module and Hull Cytogenet. Cell Genet. 90:291-297 (2000).
| Cytogenet. Cell Genet. 90:291-297 (2000).
| RMBL, AB034730; BAA22310.1; -. |
| RMBL, AB034730; BAA22310.1; -. |
| RMBL, AB034730; BAA22310.1; -. |
| RMGD, MGI:1891344; Prg4. |
| InterPro; IPR001212; Somatomedin.B. |
| R Pfam; PF00045; Hemopexin. |
| R PRINTS; PR00021; SOMATOMEDINB. |
| R SMART; SM00120; HX; 2. |
| SMART; SM00120; HX; 2. |
| SMART; SM00120; HX; 2. |
| R PROSITE; PS00024; HEMOPEXIN; UNKNOWN 1. |
| R PROSITE; PS00524; SOMATOMEDIN B; 2. |
| SEQUENCE 1054 AA; 115991 MW; 4FC64BFA42283235 CRC64; |
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                                                                       ^{Y.;}_{\text{the}}
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                                                               Ikegawa S., Sano M., Koshizuka Y., Nakamura "Isolation, characterization and mapping of
                                     SEQUENCE FROM N.A.
MEDLINE=20573856; PubMed=11124536;
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Matches 773; Conservative
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Mus musculus (Mouse).
Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-OCT-2000 (TEBMBLrel. 15,
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01-MAR-2004 (TEMBLE).
Mus musculus.
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MEDLINE-99120896; PubMed=9920774;
MEDLINE-99120896; PubMed=9920774;
Plannery C.R., Hughes C.E., Schumacher B.L., Tudor D., Aydelotte M.B.,
Ruettner K.E., Caterson B.;
"Articular cartilage superficial zone protein (SZP) is homologous to
"Articular cartilage superficial zone protein protection is a multifunctional
megakaryocyte stimulating factor precursor and Is a multifunctional
proteoglycan with potential growth-promoting, cytoprotective, and
lubricating properties in cartilage metabolism.";
                                                                                                                                                                                                                                                                                                                                                                                        ------EIONKPEETTPASEDSDD
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                     PITLKEPAPITPKKPAPKELAPITIKEPISITSDKPAPITPKGTAPITPKEPAPITPKEP
                                                                                                      731 APTIPKGTAPITLKEPAPITPKKPAPKELAPITIKGPISITSDKPAPITPKETAPITPKE
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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MEDLINE=94132002; PubMed=8300571;
Gum J.R. Jr., Hicks J.W., Toribara N.W., Siddiki B., Kim Y.S.;
Gum J.R. Jr., Hicks J.W., Toribara N.W., Siddiki B., Kim Y.S.;
"Molecular cloning of human intestinal mucin (MUC2) cDNA.
Identification of the amino terminus and overall sequence similarity
to prepro-von Willebrand factor.";
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                 "Immunodetection and partial cDNA sequence of the proteoglycan superficial zone protein, synthesized by cells lining synovial
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23.4%; Score 1714.7; DB 2;
Best Local Similarity 80.2%; Pred. No. 4.1e-28;
Matches 320; Conservative 24; Mismatches 52; ;
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Commun. 254:535-541(1999)
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                                                                              TISSUE=Articular cartilage;
MEDLINE=99171663; PubMed=10073655;
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EMBL, AF056218; AAD13404.1; --
InterPro. 1PR000585; Hemopexin.
Pfam; PF00045; Hemopexin; 2.
SMART; SM00120; HX; 2.
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518; Indels 1254; Gaps
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                                                                                                                                                       MEDLINE-91358717; PubMed-1885763;

MEDLINE-91358717; PubMed-1885763;

A Toribara N.W., Guu J.R. Jr., Culhane P.J., Lagace R.E., Hicks J.W., REDLINE-91358717; PubMed-1885763;

A Toribara N.W., Guu J.R. Jr., Culhane P.J., Lagace R.E., Hicks J.W., R. W.C.-2 human small intestinal mucin gene structure. Repeated arrays and polymorphism.", Calin. Invest. 88:1005-1013(1991).

I. Clin. Invest. 88:1005-1013(1991).

I. FUNCTION: Coats the epithelia of the intestines, airways, and other mucus membrane-containing organs. Thought to provide a protective, lubricating barrier against particles and infectious of the mucosal surfaces.

SUBUNIT: Multimeric.

I. SUBCELLULAR LOCATION: Secreted.

I. SUBCELLULAR LOCATION: Secreted.

I. SUBCELLULAR LOCATION: Secreted.

I. TISSUE SPECIFICITY: Colon. Small intestine, colonic tumors, bronchus, cervix and gall bladder.

Interchain disulfide bonds (By similarity).

I. POLYMORPHISM: The number of repeats is highly polymorphic and interchain disulfide bonds (By similarity).

I. SIMILARITY: Contains 1 TiL (Trypsin inhibitory-like) domain.

I. SIMILARITY: Contains 2 VWFC domains.
                                                                                                 "The human MUC2 intestinal mucin has cysteine-rich subdomains located both upstream and downstream of its central repetitive region."; J. Biol. Chem. 267:21375-21383(1992).
                                         TISSUB=Colon;

MEDILINE=93016075; PubMed=1400449;

Gum J.R. Jr., Hicks J.W., Toribara N.W., Rothe E.-M., Lagace R.E.,

Kim Y.S.;
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Mucin 2.
APPROXIMATE REPEATS.
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                           SEQUENCE OF 626-1895 AND 4196-5179 FROM N.A.
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PROSITE; PS01185; CTCK 1; 1.
PROSITE; PS001225; CTCK 2; 1.
PROSITE; PS01202; EGF 1; UNKNOWN 1.
PROSITE; PS01208; VWFC 1; 2.
PROSITE; PS50184; VWFC 2; 2.
Glycoprotein; Repeat; Signal.
Biol. Chem. 269:2440-2446(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR006209; Cysrich TIL.
InterPro; IPR006209; Cys knot.
InterPro; IPR006209; Cys knot.
InterPro; IPR006209; EGF_like.
InterPro; IPR001007; WWF_C.
InterPro; IPR001846; WWF_D.
Pfam; PF00007; Cys knot; I.
Pfam; PF00009; WWC; I.
Pfam; PF000094; VWC; I.
SMART; SM00041; CT; I.
SMART; SM00214; VWC; Z.
SWART; SM00214; VWC; Z.
SWART; SM00214; VWC; Z.
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Potential) Potential (Potential) (Potential)

(Potential) Potential) 48

DOMAIN REPEAT REPEAT

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RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Eshers R.P., George R.A., Lewis S.E., Holt R.A., Eshers R.B., George R.P., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Mannatides D.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.C., Rogers Y.H., Blazej R.G., Champen M., Pfeiffer B.D., RA Brandon R.C., Rogers Y.H., Blazej R.G., Champen M., Pfeiffer B.D., RA Brallew R.M., Basul A., Baxendale J., Bayraktaroglu L., Basaley E.N., Barli J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Basaley E.M., Barli J.F., Bonds J., Borchan B.P., Bhandari D., Bolshakov S., RA Berson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S., RA Berson K.Y., Cawley S., Dahlke C., Davenport L.B., Daviss P., RA Berson K.Y., Cawley S., Dahlke C., Davenport L.B., Daviss P., RA Berris K.C., Busam D.A., Butler H., Cadieu E., Center A., Coup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Borson K.J., Evangelista C.C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., Ferrac C., F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaser (Fruit fly).

Bukaryota, Metazoa, Arthropoda; Hexapoda, Insecta; Pterygota,
Neoptera, Endopterygota, Diptera; Brachycera; Muscomorpha;

Bphydroidea, Drosophilidae; Drosophila.
1120 VAFRGHYFWMLSPFSPP-----SPARRITEVWGIPSPIDT 1154
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60; 61 KRVCTABLSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP 120 121 PPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEVKDNKKNRTKKKP-ŢPKPPVVDEA 179 169 -----CSEESSTAIPSSPCIDISTVIPISPCTOETTPPTCSTOGTQTTPCTCAQTT-- 221 327 9 20 263 385 323 383 468 443 SEQUENCE FROM N.A.
MEDLINE-22426075) pubMed=12537573;
Kaminker J.S., Bergama C.M., Kronmiller B., Carlson J., Syller Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
"The transposable elements of the Drosophila melanogaster." 10 LLLLLSVFVIQQV-----SSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF 72 RP----KSTRRTTKRT-KRPRRKTTKWTTK----RATKRTTKRTTRRRPTTPKTP----180 GSGLDNGDFKVTTPDT-----STTQHNKVS----TSPKITTAKPINPRPSL ------NPTTTKPROKTK 118 ----DITDSPITTTGAECTCSDRTTASSIDSTIDRTIVINIDWITPLCIDIPPCT----222 PPNSDISKETSLIVNKETIVE------TKETITINKQISIDGKEKI--TSAKETQS 6 IFLTVSILLÍQVKNVKANYDWDSMQD------GPSEEIIPGCGGDTIYY----PD-222 -------TİPRSTİİTSİSRPITIİPRSTITITISRPITIİPRS 264 TRRPTİTTPRCTTİTSTCAPTTİTPRSTTTİTİSRPTTİTPRCTTTTSTCSPTRİTPRST MEDLINE-22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
Bettemcourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., 328 IKSAPTIPKEPAPTITKSAP--TTPKEPAPTITKEPAPTIPKEPAPTITKEPAPTITKSA 270 IEKTSAKDLAPTSKVLAKPTPKAETT---TKGPALTTPKEPTPTTPKEPASTTPKEPTTT PTT-PKEPAPTTP-------KKPAPTTPKE-----PAPTTPKE----PT 324 TITSTSRPITITPRCTTTPSTTCTRRPITITPRSTTTTCTSGPTTTTPRSTTTTCTSGPT 418 PITPKEPAPT-TKEPAPTTPKEPAPTAPKKPAPTTPKE-----PAPTTPKEPAPTTT 384 TitipRSTTTTSTSGPTTTTPRSTSTTTTTPRSTTTTTSTSGPTTTTPRST Gaps 18.9%; Score 1381.2; DB 2; Length 1225; 25.5%; Pred. No. 2.8e-20; ive 132; Mismatches 434; Indels 548; "Annotation of the Drosophila melanogaster euchromatic genome: A99AF9D4404C79F4 CRC64; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002). ---PVQPCDTDS--EMBL, AE003575, AAF50957.3; -... FlyBase, FBGN0003372; Sgsl. SEQUENCE 1225 AA, 127735 MW; Conservative 132; Query Match Best Local Similarity Matches 382; Conserv SEQUENCE FROM N.A. SEQUENCE FROM N.A. review Lewis S.E.; systematic FLYBASE ð 엄 à ð g g ö g à Db δ g ò g à

Drosophila melanogaster (Fruit fly)

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REPENDENCE FROM N.A.

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

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RA, Amataides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

BA, Cacorge R.A., Lewis S.E., Fichards S., Ashburner M., Henderson S.N.,

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BRA, Brandon R.C., Rogers Y.H., Blazel R.G., Champe M., Peilifer B.D.,

RA, Ballew R.M., Bason B.W., Barandale J., Ballame M., Peilifer B.D.,

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RA, Bernon K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,

Berkova D., Betchan M.R., Bulke C., Davenport L.B., Borteter P., Chandra I.,

RA, Berlos B., Pelcher R., Domes Z., Mays A.D., Dew I., Dietz S.M.,

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RA, Durbin K.J., Evangeliste C.C., Ferraz C., Ferriers S., Punkov B.C., Gabriellan A.B., Galbart W.M., Classer R.,

RA, Godorn K., Obup L.E., Downes M., Dugan P., Harris M.,

RA, Harris N.L., Havrey D., Heiman T.J., Hernandez J.R., Houck J.,

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RA, Mannel B.E., Kodire C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

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RA, Mallai M., Moy M., Murphy B., Murphy L., Murzny D.M., Nelson D.L.,

RA, Rainer K., Melson N., Stupleron M., Stung K., Santh T.,

RA, Spier E., Stepleron K., Saunders R., Weissenbach J.,

RA, Spier E., Spradling A.C., Stapleton M., Strong R., Suh B.,

RA, Shen B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith T.,

RA, Shen E.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith H.O.,

RA, Shen E.C., Shender S., Subner S., Shen H.,

RA, Shen S., Work M., Work M., Weissenbach S.,

RA, Shen S., Solaner S., Robin M., Sheng
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
                                                                                     Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Bucoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., RA Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P., RA Harris N.L., Richter S.E., de Grey A.D., Drysdale R.A., RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., RA Lewis S.E., Lewis S.E., RA Lewis S.E.	18.3%; Score 1339.8; DB 2; Length 1761; 24.1%; Pred. No. 4.1e-19.	ESPERGRECDCDAQCKKYD:	DD 5 CF1WLALYHSANAALEGSEIKFGDESTTESAEKYPDYCWI 44 QY 108 HNPTSPESSKKAPPPSGASQTIKSTTKRSPRNPKKKYTKKVIESFETTFVKNNKK 163	TTLKITIKSTAK		204SISPKITTAKPINPRPSLPPNS	TTTIKSTSELITTLK	VY Z5/ GKEKITSAKETQSIEKTSAKDLAPISKVLAKPIPKAETTTKGPALTTPKEPT 308	309PTTPKEPASTTPKEPT	Db 253 KSSTAKTTREPTTKRETTERTTKEPSTSKTTTHETTAEPATKKTTHEPTTQKSTTLRITE 312		513 BF11KKDSIAKITKEPITKRETTERTTÖEPSTSKTKTHETTAEPATKKTTHEFTTOKSTT 372 QY 347 PITPKEPAPITTKEPAPITPKEPAPITTKRPA	SKTTTHETAAEPATKKTTHEP		КТКТНЕТТАЕРАТКК		: : ERTTQEPSTSKTTTHETTAE		ISKTTTH	Qy 473	DD 611 ETTAEPATKKTTHEPTTQKSTTLRITEEPTTRKSSTARTTREPTTKRETTERTTQEPSTS 670
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082 ATKKTTHEPTTQKSTTLRITEBPTTRKSSTAKTTREPTTKRETTERTTKEPTTHK 1141 671 KITTHETTABPATKKTTHEPTTQKSTTLRITEEPTTRKSSTAKTTREPTTKRETTERTTK 730 731 БРТТКИТТНКТТБЕРГТККТТНЕРТТККSTTLКРТЕЁРТТККSTTKTBPTTREPTTKKTT 790 906 197 PITRKITIHKITEEPITNKITIKKITHEPTİKKSTILKPIEEPITRKISİİKTİREPİİK 1256 |:| ||:|| ||:|| ||::| :| :| || ||::| ||::| ||::| ||::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||: ----PITPKEPSPITIK 515 566 791 BRİTKEPTTRKTTTHKTTEEPİİNK----İTİKKTTHEPİTKKSTTLKPTEEPTTRKTST 846 586 -PEKLAPITPEKPAPITPEELAPITPEEPT------PITPE---EPA----- 622 907 RKSSTÄKTTRE---PTTKRETTERTTKEPTTRKTTTHKTTEEPTTKKTTHEPTTKKSTTL 963 ----PITPKAAAPNTPKEPAPITPKEPAPITPKEPA------PITPKETA--- 662 663 ---PITPKGTA-----PITLKEPAPTTPKKPAPKELA-----PITTKEPTSTKSPKP 706 707 A-----PITPKGIA-----PITPKEPAPTIPKEPA-------PITPKGIAPT 741 742 TLKEPA-----PTTPK----KPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKE 790 376 TEEPTTRKTSTTKTTREPTTKRVITERTTREPTTRKTT--THKTTEEPTTKKTTTTKKTTH 1433 434 EPTIKKSTILKPIEEPTIRKISITKTIREPITKRVITERIIREPITRKTITHKITEEPIT 1493 791 PA-----APTIPETPEPTIS 812 990 -----STKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAE 1027 |----KPTEEPTTKKTTTKKTTHEPTTKKSTTL----KPTEEPTTRKTSTTKTTREPTTRETS 1609 510 TSVKÍTADOTTKRITAEMSITNQEÞÍSVETITNSSNOSNITTESTÍTEBOHVHHHHHHH 1669 813 EVSTPTTKEP----TILHKSPDE-----STPELSAEPTPKALENSPKEPGVPTTKTPA 862 893 ------KMIKETAI---TIEKTIESKIJATIJQVISTITQDTIPFKIJTLKI-- 935 863 ATKPEMITTAKDKITERDLR----------TIPETTIAAP 892 936 -----TILAP-----KVTTIK-----KTITTTEIMNKP------EETAKPKD 966)63 -HMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVA 1121 535 PTTPKEPA------EPTTPKEPAPTTTKKPA--PTAPK------EPA--||| :|| 847 TKITRBPTTKRBTTERTTQEPSTSKTTTHBTTABPATKKTTHBPTTQKSTTLRITEBPTT ----PTTPKKL,T-----PTT. 128 AMLQTT-----TRPNQTPNSKLVEVNPKSEDAGGAEGETP---967 RATNSKATTPKPQ-----KP-----TKAPKKPT----70 YH---KPADLGPSILP----LPDLP---------PITPKETA----------TTKEPA-490 516 623

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                                                              1182 DAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGR 1241
                                                                                                                          1242 RPALNYPVYGEMTQVRRRRFERAIGPSQTHTIRIQYSPARLAYQDKGVLHNEVKVSILWR 1301
                                                                                                                                                         1725
1122 FRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDIK 1181
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Last annotation update)
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SEQUENCE FROM N.A.

MEDLINE=22426065; PubMed=12537568;
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Matches 482; Conservative 106; Mismatches 399;
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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DD 1376 TEEPTTRKTSTTKTTREPTTRKTTT-THKTTTETMINGP 966 1434 EPTTKKTTTRAPKVTTK	NEBSULT 11
332 -PTTPK	Db 907 RKSSTAKTTRE—-PTTREETAPTPEEPPT—

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	336KEPAPTITKEPAPTIP	372 TTIKEPAPITTKSAPITPKEPAPITPKKPAPITPKEP 408	409 APTYPKEPTPTYPKEPAPTTYEF 430		470 EPSPTTPKEPA 490 70 EPSPPITTKSAPTT 490 788 EPSTTPGTRITPTRAFFSTESTDTTMSSASTSEPSTTFGTTRITPTRAFFSTESTDTTMSS 847	TKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPAP :	528TIPKKPAP 543 1			581 LTPTTPEKKLAPT	TPETPEBLAPTTPEBLAPTTPEBLAPTTTPE	1148 TPTRPTSTESTDTTMSSASTPEPSTTPGTTRTTPTRTFTSTESTDTTMSSASTPEPSTTPG 1207	TTRTTPTRPISTESTDTTMSSA	GTRITIPREFICESTDITMSSASTPEPSTTPGITRTSPTRPTSTESTDTTMSSASTPEP GTRITIPREFICESTDTTMSSASTPEPSTTPGITRTSPTRPTSTESTDTTMSSASTPEP	TIPELANITATION TATA TATA TATA TATA TATA TATA TATA TA	DITMSSASTPEPTITEGITRITETRESTDI	723PAPITPKGTAPITLKEPAP '48 13	7497TPKKPAPKELA749 T60 749	
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	121 IQYIYKQEPVQKCEGRRPALNYPVYGETTQVRRRRFERAIGPSQTHTIRIQYSFARLAY 180 1285 QDKGVLHNEVKVSILWRGLPNVYSAISLEDNIRKPDGYDYYAFSKDQYYNIDVPSRTARA 1344			LT 12 DS QTPMDS PRELIMINARY; PRT; 3150 AA.	V.Fmil.5; 01-MAR-2004 (TrEMBLrel. 26, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) ENSANGPO0000004655 (Fragment).	Name=ENSANGG000000003651; Anopheles gambiae str. PEST. Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles. NYTT TAXTD=180454;	[1] ————————————————————————————————————	Anopheles Genome Sequencing Consortium; submitted (APR-2003) to the EMBL/GenBank/DDBJ databases. -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is	preliminary data. EMBL; AARB0100890; EAA13969.2; GO; GO:0016020; C:membrane; IEA. GO; GO:0004872; F:receptor activity; IEA.	GO; GO: 0008151; F: Cell growin and Or maintenancy, ref. InterPro; IPR006770; OGF_recept. Fram, PF04680; OGF_III; 80. NON WER 1	NON_TER 3150 3150 32879 MW; 3C7B3D441CE8C839 CRC64; SEQUENCE 3150 AA; 322879 MW;	nery Match 17.9%; Score 1310.1; DB 2; Length 3150; set Local Similarity 19.1%; Pred. No. 5.1e-18; strings 465; Conservative 130; Mismatches 490; Indels 1349; Gaps 96;	110 PISPPSSKKAPPPSGASQTIKSTIKKSPKPPNKKKVIESEBITEVKDNKKN 163	141 FIREFEDITIONALITY FOR THE STREET TO BE S	OHNKVSI			369 PEPSTIPGTIRTIPTRPISTESTDTTMSSASTPEPSTIPGTIRTTPTRPISTESTDTTMS 428 295TIKGPALTIPKEPIP	SASTPEP

: : 566 ESTDTIMSSASTPEPSTTRTTPTRPTSTESTDTIMSSASTPEPSTTRGTTRTTPTR 1625		1626 PTSTESTDTTMSSASTPEPSTTPGTTRTTPTRPTPTDTTMSSASTPEPSTTPGTTRTTPT 1685	798 KPAPTSEVSTPTTT 820	KEDTITIHKSD		2 6	PEPSITEGITRIPERFISIESTOTIMSSASTPEPSITEGITRITPIRFISIESTOTIMS		6 SASTPEPSTIPGTIRTIPIREPISIESTDTIMSSASIPEPSTIPGTIRITPIRPISIESTD	900 TTTIPRITESKITATITQVISTITQDTIPPKIT 931	TIMSSASTPDPSTIPGTIRTTPTRPTPTRTIMSSASTPEPSMIPGTIRTTPTRPTSTEST		DITMSSASTPEPSTIPGTIRITPIRP - ISTERIDITMSSAYTPEPSTIRGITRITPIRP	5KDRATNSKATTPKPQARPTKAPKK		PISTKPKTMPRVRKPKTTPTPRK		MTSTMPELNPT-SRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHV	TIPIRPTPIDSIMSSSMSSASITPGTTRITPIRPISTESTDITMSSASIPE	11 FMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWML 1130			: : :	PKPIF	: : : :	YIYKQEPVQKCPGRRPALNYPVYGEMTOVRRRR	PIPQCRLVCRQPLLRSHPRHLVQPELLQQDQHLPIPQCRQPLLRSH	FERALGPSQTHTIRIQYSPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRK	LRHLVQPQELLQQDQHLPSTDTTMSSASTPE	9 PDGYDYYAFSKDQYYNIDVPSRTARAITTRSGQT 1352	4
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PRT; 3409 AA.

Q6SSE6 PRELIMINARY; PRT; Q6SSE6; 05-JUL-2004 (TrEMBLrel. 27, Created)

RESULT 13 Q6SSE6 ID Q6SSE AC Q6SSE DT 05-JU

80; 50 LAWYIIPVSDALQFPVNVSVTSSAATDAPSAIAYIGALLDVLWNVPWQPNCINDTRRSYD 109 110 APWPSRCALPAVQYGYYDETYIDATVYSGNSLRPFYSTCRYPASSDPYAFLEPYSMPWVD 169 170 DFGIYQPVLDGFDMWMGFTVNTVDSNLKWIDPAWTAQGAWLGGQDF-------RD 217 -----SSČENÝĎIA 243 16 244 DPYDPDKIANGIVPAVITALDFRNASLYIYYLDFGMFPAGSLDNVWYLNLAYNFIGGPLP 303 101 304 ANLPTLLPSLQHLALDHCRATPDVRGTASLQYGWQQYPSTGQPYBYCSDGDVTGSDGTEY 363 101 364 VISGMIPDEWGDAVAAAASDSSLPWANLRTVRLSNQALYGPIPEGLRSASSSISSWRLQG 423 -QDLSSCAGRCGEGYSRD 41 42 ATCN-----CDYNCQHYMECCPDFKRVCTAELSCKGRCFESFERGRECDCDAQCKKXD-- 94 | | | ::: 424 NTELCGPLPEFAAPINSLLYLGTKLGTHTWVMHDPADHTQGGECLAPPPPSPPSPPSPR 483 ----- 128 484 PPPLPPSPPPPLLPPSPPVPPPSPPSPPSPPPSPPEPPSPPLPPSPPSPTPVARCIOVG 543 -----IKSTTKRSPKPPNKKKTKKVIESEEITEVKDNKKNRTKKRTP 171 172 KPPVVDEAGSGLDNGDFKVTTPDT---STTQHNKVSTSPKITTAKPINPRPSLPPNSDTS 228 620 289 TPKAETITIKGPALITPKEPTPTTPKEPAST-----TPKEPTPTTIKSAPTTPKEPAPT 341 Chlamydomonas reinhardtii.
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X [6]—AxID Lau J., Gaps 229 KETSLIVNKETIVETKETITINKQISTDGKEKTISAKETQSIEKTSAKDLAPTSKVLAKP -----FHPPSPDSPASSVPPSPRPPSPRPPSPAPPSPAPPSPP---------PRAPRP ----PPSPAPPSP 17.2%; Score 1256.8; DB 2; Length 3409; 14.0%; Pred. No. 7.5e-17; tive 166; Mismatches 460; Indels 1812; -----YLLLLLSV-----Last sequence update) Last annotation update) --PTSPPSSKKAP-AVWNFGTHYCSW---PFVEC-----102 ----SFCAEVHN------------FVIQQVSS-----1 MAWKTLPI------Conservative 05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel. Plus agglutinin. Name=SAG1; Similarity 110 -----Query Match Best Local Simi Matches 398; 579 SPP-17 17 95 95 102 129 qq ð g δ ò g δ g ð g qq ð à gg ò g ò Db ð g ò g à q

ID	AAS07044 PRELIMINARY; PRT: 3409 AA.		
AC	BLrel. 27, Created)	qa	630 APPSPAPPSPQPPSPVPPQI
555	02-MAR-2004 (TrEMBLrel. 27, Last sequence update) 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)	δ	342 TTKSAPTTPKBPAPTTTKEPAPTTP
388	Files agglutinin. SAGI	qu	684 PPNPAPPSPAPPLPPSPEPPSPAPP
3008	Cnlamydomonas reinhardtii. Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.	Qy da	398 KKPAPTTPKEPA : : : 744 RPDCDADBCDERGRANDICAL
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Z Z Z	SECTOR D. T., Waffenschmidt S., Umen J.G., Ishida K., Kubo T., Lau J., Goodenough U.W.:	Z 63	
RL	"Plus and Minus Sexual Agglutinins from Chlamydomonas reinhardtii."; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.	δ	
SQ	EMBL; AY450930; AAS07044.1; - SEQUENCE 3409 AA; 336045 MW; 7FE87633EDD6631F CRC64;	qa	: : :
On Be Ma		& A	528TTPKKPAPTTPKEP
λŏ	1 MAWKTLPI	ò	564EPAPTTPKETAPTT
qq		셤	: 383 PPSPAPPSPDPPSPAPPSPAPPSPNP
λ		λö	609
QC	110 APWPSRCALPAVQYGYYDETYIDATVYSGNSLRPFYSTCRYPASSDPYAFLEPYSMPWVD 169	qu	1042 PPPPPEPPSPEPPSPAPPLPPSPEP
δλ		δò	649 TPKEPAPTTPKETAPTTPKGTA
qq		eg G	1102 PPSPEPPSPAPPSPSPPAPPSPEPPS
à	42 ATCNCDYNCQHYMECCPDFKRVCTAELSCKGRCFESFERGRECDCDAQCKKYD 94	δλ	675KEPAPITPKKPAPKELAPIT
Dp	218 AVWNFGTHYCSWPFVECSSCENYDIA 243	qq	1162 PPTPPPSPAAPPSPQPLEPS
δλ	96	λõ	705 KPAPTTPKGTAPTTPKBPAPTTPKEP/
Dp	244 DPYDPDKIANGIVPAVITALDFRNASLYIYYLDFGMPPAGSLDNVWYLNLAXNFIGGPLP 303	QQ	1222 SPAPPSPAPPSP-APPSPAPPSPAPPS
٥'n	95KCCPDKCCPD	δλ	764 TKGPTSTTSDKPAPTTPKETAPTTPK
QQ	304 ANLPTLLPSLOHLALDHCRATPDVRGTASLQYGWQQYPSTGQPYEYCSDGDVTGSDGTEY 363	qq	1277 SPAPPSPAPPSPAPPSPAPPSPEI
οχ	102 101	δ	823 PTTIHKSPDESTPELSAEPTPKALE-
QQ	364 VISGMIPDEWGDAVAAAASDSSLPWANLRTVRLSNQALYGPIPEGLRSASSSISSWRLQG 423	qq	1334 PLPPSPAPPLPVPPASPAPSPSPLRP
δy	102SFCAEVHN 109	ζŏ	859 KTP
qq	424 NTELCGPLPEFAAPINSLLYLGTKLGTHTWVWHDPADHTQGGECLAPPPPPSPPSPRPPR 483	qq	1394 PTPPLAPLPPDCTLLAQAALLSIPDAA
λŏ	110 128	ò	868 MTTTAATTTA
qq	484 PPPLPPSPPPLLPPSPPVPPPSPPSPPSPPSPPSPPPLPPSPPSPTPVARCIQVG 543	qq	1454 LTATAISLVGGSSRGNNTNGSSSGGNY
δ	129IKSTTKRSPKPPNKKKTKKVIESEEITEVKDNKKNRTKKKPTP 171	δλ	873KDKTTERDL
ПЪ	544 GICDSPSPMPPSPRPPQPPSPRPPPPPPPPP	Dp	1514 GPGTETAAEWAVDAVQDGTYQLQLSIG
Qy	172 KPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTS 228	δλ	886
Dβ	579 SPPFHPPSPDSPPASSVPPSPPSPRPSPAPPSPAPPSPP 620	Пр	1574 AVGEASLNALGSKQAMLLTISFSEPVP
à	229 KETSLIVNKETTVETKETTTTINKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKP 288	δŏ	896KETATTTEKTTESKIT
Dp	621	අු	1634 LPAELVATAAGSSSSSGTSRSGNGNGT
δy	289 TPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPT 341	ò	912

SPAPLLPPSPDPPSPAPPSPMPPPLPTSPPSPSPV 1161 | : | : | : | | : | OPPSPAPPSPAPSPA 683 PK----EPAPTTTKEPAPTTTKSAPTTPKEPAPTTP 397 РАРТТРКЕРТРТТРКЕРАРТТКЕРАРТТРКЕРАРТ- 442 SPEPPSPAPPSPAPPSPAPPSPEPPSPEPPSPEPP 1221 APT-----TTKE 470 SEPAPTTPKAAAPN-----TPKEPAPTTPKEPAPT 648 SPAPPSPFPPSPQPPSPEPPSPAPPSPVPPSPAPPS 863 APTTTKSAPTTPKEPSPTTTKEPAPTTPKEPAP--- 527 SPAPPSPAPPSPEPPSP APPSPAPPSPOPPSPEPP 922 TPKKLTPTTPEKLAPTTPE--KPAPTTPEELAPT- 608 PPQPQTPAMPPPSPAPPSPAPPSPAPPGVPPPPT 1393 AANSVFVVSAGLPTSVAPSTPPELLASFCTVCSCQ 1453 NYYSNGGDAAIQRIPAGNSTDRGGSSSGSGGSSSW 1513 SPAPITPKEPAPITKKPAPIAPK------ 563 ----TKEPTSTTSD 704 PAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPT-T 763 KEPAPITPKKPAPITPETPPPT-ISEVSTPITKE 822 GGVTYTRTVVVDRTPPSVSGNVTLSANRIKQEPS 1573 PAFDPAASLIVTGALVAEWVAAADKMTFYVLAMT 1633 TAAAAAAAAPPPPAGTTGRRRALQQQAAAPPPPA 1693 -----NSPKEPGV---PTT 858 ----- ETTTAAPKMT----- 895 --------AATKPE------------RTTP-----APTTL

612 ----EPTSPPQPPPPAPPSPPSPPTTPDVPPMPPSSPPAPVMPPAPPPQPPIPPASPLT 667 ---- 120 92; 372 WSAEYAQALSYVRDGSQLRPRGWLPPVIEPVSARLLLPDTLRRLTIRRTRDEQHGAVQWT 431 | ; 432 SRPLITGPLPGEWALLRNLEYLDLSDEMETGALVGPIPSTWLMMSHLRVINMTGHHNFCR 491 492 DWHKIISWQIRMYYRAATHEPNLNVPHYYGPWGGNNGNWTRYNISVYDLSGHGWQWYDEV 551 192 GTVPTYSISGTRYRQNDTVYRIMHNGAVTNPANVTRNQVKSIKLRHSAMWHHPSVNITSP 251 252 PEFSLVSELACLPLEEIFLEDVALRADYSVLMAQPNTTLDNGKVFNLYDPSTYPFNVTGL 311 312 YNNVFSMLIEPSFMLHSSVSVKASŠFNPGLALRNAALRTCNFAPFTELHAMRWTGQAQLD 371 72 EVATRLGEGTAPWRCISNCQTQIFTSDQQCAPDCESRTYCEPGGAALGSENTTCCALSLL 131 89 95 132 DQTYASAQPPSSTQPAWCSTYPGWGARPRPSVCDFNVFAARGTTPPAGADDPDLAVSCSS 191 75 -----CK 91 65 29 SCAGRCGEG-----CC----YSRDATCNCDYNCOHYME------CC---- 57 ----PDFKRVCT- 65 71 66 -----KGRCF------22 LAFATL-----FELPDLASTQTTYGPWNATEDLNEQHKGLLAFILSGDTSFWSRP IN=CC-621, Waffenschmidt S., Umen J.G., Ishida K., Kubo T., Lau J., Fabough U.W.; Waffenschmidt S., Umen J.G., Ishida K., Kubo T., Lau J., itted (OCT-2003) to the EMBL/GenBank/DDBJ databases.; AX50292; AAS7042.1; -rpro; IPR008985; Cond. like lec_gl.
rpro; IPR008985; Cond. like lec_gl.
rpro; IPR008985; Cond. like lec_gl.
rpro; IPR008985; Pistil extensin.
rpro; IRR01414; autotrans barl; 1.
FAMS; TIGR01414; autotrans barl; 1.
FRAMS; TIGR01414; autotrans barl; 1. ch 16.2%; Score 1184.8; DB 2; Length 3889; al Similarity 12.1%; Pred. No. 3e-15; 438; Conservative 187; Mismatches 541; Indels 2452; Gaps 1 MAWKILPIXLLLLSVFVIQQVSS-----QDLS-----PPSSKKAP---Created) Last sequence update) Last annotation update) PRT; 3889 AA. 86 CDAQ-----IL-2004 (TrEMBLrel. 27, IL-2004 (TrEMBLrel. 27, IL-2004 (TrEMBLrel. 27, PRELIMINARY; 105 AEVHNPTS---------- 91 92 KYDK------------ 99 NCE FROM N.A. s agglutinin. TaxID=3055; 58 -----90 d

	DMHGNINAEPL SRSSLLQSGYH: SAGSGSGSSSSI AGUVADGSTAI NYPPPAPPPMPP STPRKMTSTMPE	DD 2241 SGSGGQQSSGASVATDTTTHTNVQDLLYTLAIAALLMVALVAAHLLVIGLWRLAVMYDVC 2300	1067 2541 1067 2601 1071 2661
121	992 PLPSPEPPSPAPPLPP		KALENSPKEPGVPTKTPAATKPE
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Search completed: October 13, 2004, 12:20:00 Job time : 199.642 secs

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protein search, using sw model 1 OM protein

October 13, 2004, 11:23:49; Search time 27.7222 Seconds (without alignments) 4723.689 Million cell updates/sec Run on:

SEQ1-G Title: Perfect score:

I MAWKTLPIYLLLLSVFVIQ......ARAITTRSGQTLSKVWYNCP 1361 Sequence:

Gapop 10.0 , Gapext 0.1 BLOSUM62 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

RESULT 1 A43932
mucin 2 precursor, intestinal - human (fragments) N;Alternate names: micin SMTC_A1
C; Species: Homo sapiens (man)
C;Date: 10-Mar-1993 #sequence revision 12-Apr-1996 #text change no.Thil-2004
C.Accession: A49963; A45106; B45106; A43932; B33532; A61257; P20328; P20329
J. Biol. Chem. 269. 2440-2444 Josa
Afithe: Molecular cloning of human intestinal micia (Mrica)
A; Reference number: A49963; MuID: 94132000: PMID: 92067: Identilication
A; Accession: A49963
A; Molecule type: mRNA
A;Residues: 1-639 <gu1></gu1>
A; Cross-references: UNIPROT: 002817; UNIPROT: 014884. GB.131000
R; Gum Jr., J.R.; Hicks, J.W.; Tortibara. N.W.; Rother F. W. 124200
J. Biol. Chem. 267, 21375-21383, 1992
A:Title: The human MUC2 intestinal minim has gretaine with miniman.
A; Reference number: A45106; MUID: 93016075. DWITD: 1400440
A;Accession: A45106
A; Status: not compared with conceptual translation
A; Molecule type: mRNA

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A/Molecule type: mRNA A/Residues: 1916-2193 <GU4> A/Cross-references: GB:MZ2405; NID:g188873; PIDN:AAA36334.1; PID:g188874 A/Experimental source: intestine R/Jany, B.H.; Gallup, M.W.; Yan, P.S.; Gum, J.R.; Kim, Y.S.; Basbaum, C.B.

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J. Clin. Invest. 87, 77-82, 1991 A: Getter Human borochus and intestine express the same mucin gene. A: Getter Human borochus and intestine express the same mucin gene. A: Getters and the compared with conceptual translation A: Getters in Commun. A: Rostdues: 77, 1925-1948, 7TS', 1952-1954 «JAN) A: Residues: 77, 1925-1948, 7TS', 1952-1954 «JAN) A: Residues: 27, 1925-1948, 7TS', 1952-1954 «JAN) A: Residues: 107, 1925-1948, 7TS', 1952-1954 «JAN) A: Residues: 2007-2016 (MID: 20198477; PMID: 1550588 Biochem Hisphys Res Commun. B: A: Rostdues: 2028-246 «XUG) A: Residues: 2028-246 «XUG) A: Residues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-246 «XUG) A: Rostdues: 2028-247 (Rostdues: 2028-247 (Rostdues: 2028-247 (Rostdues: 2028-247 (Rostdues: 2028-247 (Rostdues: 2028-247 (Rostdues: 2028-247 (Rostdues: 2028-247 (Rostdues: 2028-247 (Rostdues: 2028-247 (Rostdues: 2028-247 (Rostdues: 2028-247 (Rostdues: 2028-247 (Rostdues: 2028-247 (Rostdues: 2028-247 (Rostdues: 2028-247 (Rostdues: 2028-247 (Rostdues: 2028-247 (Ros	97 800 860 121 129 920 166 961 191

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;Date:	15-061-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004	č

----TIKSAPTTPK-----408 327 352 ò 엄상 C.Accession: T1826.
R.Fujino, T.; Beguin, P.; Aubert, J.P.
J. Bacteriol. 175, 1891-1899, 1993
A:Title: Organization of a Clostridium thermocellum gene cluster encoding the cellulosom

.us: preliminary; translated from GB/EMBL/DDBJ scule type: DNA dues: 1-1664 <FUJ> ss-references: UNIPROT:Q06852; EMBL:X67506; NID:g296879; FID:g296881; FIDN:CAA4784 85, ---FDPEVLQPVDPATGEEFTDKSMPVNRVLLTNSKYGPTPV-AGNDIKSGIINFATGYN 125 126 NLTAYKSSGIDEHTGIIGEIGFKVLKKONTSIRFEDTLSMPGAISGTSLFDWDAETITGY 185 -----KVIESBEI------TEVK------DNKKN------RTKKKPT- 170 246 LEAIELETGSAIAKRIWPVTGGTVLQSDNYGKITAVANDVGAGIINFAEAYSNLTKYRET 305 306 GVABETGIIGKIGFRVLKAĞSTAIRFEDİTAMPGAIEGTYMFDWYGENIKGYSVVQPGEI 365 37 66 -----STTQHNKV 203 229 366 VAEGREPGERPTEEPVPTETPTVTEEPVPSELPDSXVIMELDKTKVKVGDIITAT 425 230 -----ETSLTVNKETTVETKETTINKQTSTDGKEKT 261 426 IKIENWKNFAGYQLNIKYDPTMLEAIELETGSAIAKRTWPVTGGTV-----LQSDNYGKT 480 -----AKETQSIEKTSAKDLAPTSKVLAKPTPKAET 294 TT-----KGPALTTP-----KEPTPT-TPKEPASTTPKEP 323 596 VPSELPDSYVIMELDKTKVKEGDVIIATIRVNNIKNLAGYQIGIKYDPKVLEAFNIETGD 655 656 PIDEGTWPAVGGTILKNRDYLPTGVAINNVSKGILNFAAYYVYFDDYREEGKSEDTGIIG 715 116 NIGFRVLKAEDITIRPEELESMPGSIDGTYMLDWYLNRISGYVVIQPAPIKAAS----D 770 EPAPITIKEPAPITEKEPA----PITIKEPAPITIKSAPITEKEPAPITEKEPAPITEKE 407 ----EPAPTTTKSAPTTPK 351 ------FAEATPSIEMV 59 ------DFKRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPD ------PSSKKAPPPSGASQTIKS------4 KTLPIYLLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCP----Gaps 204 ------STSPKITTAKPINPRPSLP-----PNS-----DTSK-----Y Match
16.1%; Score 1179; DB 2; Length 1664;
Local Similarity 20.9%; Pred. No. 4.4e-17;
thes 412; Conservative 138; Mismatches 460; Indels 960; rence number: Z18847; MUID:93209931; PMID:8458832 ssion: T18262 38 LDKTEVHVGDVITATIKVNNIRKLAGYQLNIK-----6 KVLSILLILLL----IISTTSVNMS--------TTKRSP-----KPPNKKKTK----GDFKVTTPDT 100 YESFCAEVHNPTSP---327 -----324 TPT----262 TS----132 171 186 295

947	A   A   A   A   A   A   A   A   A   A	670 1106	TTPKE 729 Query Ma :-   Best Loc :DE 1161 Matches	'KETAP 785 QY :   Db 5			1319 DD 964 QY		3SGGSG 1401 Db	106	1449	1461 Db		1491	1547	QQYIYKQ 1232 QY	NYIKRS 1605 Db	KGVLHN 1292 QY	Db	9		λo
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Qy 454 Db 891 Qy 513	Db 9 Qy 5 Db 10	Oy 615	Qy 671 Db 1107	oy.		a ko	Db 1.		Qy Db	Qy 101		UV T	Qy 1		. F			ζ		λö	qa	

preliminary; translated from GB/EMBL/DDBJ e type: mRNA ss: 1-7962 <RES> eferences: UNIPROT:Q10465; EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g101 5959 KPAPEEVAPVPIPKKVBPPAPKVPEVPKKPVPEKKPVPVPKKEPAAPPKVPEVPKKPVP 6018 5695 5718 5719 AVYEKKQAVHKEKRVFIESFEEPYDELEVEPYTEPFEQPYYEEPDEDYEEIKVEAKKEVH 5778 5839 APPPRVIKKPVIEKIEKIEKTSRRMEEEKVQVTKVPEVSKKIVPQKPSRTPVQEEVIEVKVP 5898 5899 AVHTKKMVISEEKMPPASHTEEEVSVTVPEVQKEIVTEEKIHVAVSKRVEPPPKVPELPE 5958 5596 317 STIPKEPIPITI-----KSAPITPKEPAPITIKSAPITPKEPA-----PITIKEPAP 363 5420 ILKEGOICTMTVQFSVPNVKSEWFRNGRILKPQGRHKTEVEHKVHKLTIADVRAEDQGQY 5479 5597 LKPPDIPDSRVPIÞÍMÞIRAVPPEEIPPVVAPPVPLLLPTÞEBKK-ÞÞPKRIBVTKKAV- 5654 179 AGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKE 238 253 -----EPTPTTPKEPA 316 107; 134 KRSPKPPNKKKTKKVIES-----EEITEVKDNKKNRTKKKPTP------KPPVVDE 178 ----EKTSAKD 277 62 5537 ELTESQKYNFRNDGRCHYMTIHNVTPDDEGVYSVIARLEPRGEARSTAELYLTTKEIKLE ----PSSKKAPPPSGASQTIKSTT --------SKABEVKIMT---ITRKK----------EVQKB-----KE ltin - human (fragment)
: Homo sapiens (man)
9-May-1998 #text_change 09-Jul-2004 ch 14.5%; Score 1061.2; DB 2; Length 7962; ll Similarity 15.1%; Pred. No. 4.2e-13; 439; Conservative 129; Mismatches 510; Indels 1828; Gaps -----PDFKR------------NHA---4 KTLPIYLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDY------STDGKEKTTSAKETQSI------SCKGRCFESFERGRECDCDAQCKKYDK-----CCPDYESFCAE-----HXMECC---eferences: GDB:127867; OMIM:188840 ition: 2q31-2q31 239 TIVETKETITINKOT-----------PTSP----278 LAPTSKVLAKPT-PKAETTT 300 ALTTPK---------VCT---254 ----DB:TIN 5655 110 9699 63 107 4 69 8 8

733 760 760 7156 807	WAY   B54 GVPTT	7467 KKPVLEEKPAVPDERAL 995KTMBRVBA 7527 PEEPKKIIPEKKVPVIKK 1008	1086 PWGGIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSBARFKG 7758  1086 PWGGIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSBPSPARR 1141  7759
TTPKEBAPTTTKEBAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEBA 409  -EEKI PUPVAKKKEAPPAKVPEVQKGVVTEEKITIVTQREESPPAVPEIPKKKVPEERK 6077  FTTPKEPTPTTPKEPAPTTK-EPAPTTPKEBAPTA	APTTPKEPAPTTPKE 462	554 6497 565 6557 616 616 6676	LIPE 6735 684 LPEE 6795 687 698 698 TTP 727 TYP 727 732 732 LEEV 7095

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130820 nascent polypeptide-associated complex alpha chain, muscle splice form gp220 - mouse N.slternate names: alpha-NAC protein	රි ස්	TLATSIPK 8
es: Mus musculus (house mouse) 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004	2 6	
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A;Molecule type: DNA A;Residues: 1-2187 <yot> A;Cross-references: UNIPROT:P70670; EMBL:U48363; NID:g1666688; PID:g1666689; PIDN:AAB187</yot>	ð í	464 APTITKEPSPTTPKEPAPT-TTKSAPTTTKEPAPTITKSAPTT 505   :
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424 THVPPPTSSGLVSSKDPASPVTSLVVPAAHKQFPAPPASATLGVPVSPLPA 474	3 8	
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Cyst germination specific acidic repeat protein precursor - Phytophthora infestans CiSpecies: Phytophthora infestans (potato late blight agent) CiBate: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004 C;Accession: T31108 R;Goernhardt, B. Submitted to the EMBL Data Library, April 1998 A;Reference number: 220986 A;Acteroscion: T31108 A;Actatus: preliminary; translated from GB/EMBL/DDBJ A;Gutus: preliminary; translated from GB/EMBL/DDBJ A;Gutus: preliminary; translated from GB/EMBL/DDBJ A;Gutus: preliminary; translated from GB/EMBL/DBJ A;Gutus: preliminary; translated from GB/EMBL/DBJ A;Gutus: preliminary; translated from GB/EMBL,ApGI185; NID:G3851513; PID:G3851514; PIDN:AAC7 C;Genetics: A;Genetics: A;Genetics:	<pre>Query Match 14.0%; Score 1027.3; DB 2; Length 1489; Best Local Similarity 24.2%; Pred. No. 6e-14; Matches 430; Conservative 67; Mismatches 452; Indels 827; Gaps 84;  41 DATCNCDYNCQHYMECCPDFKRVCTABLSCKGRCFESFERGRECDCDAQ 89                                      </pre>	LLSYNGAVCVAPVDAECALIHDDMWGCEFPKTGYTSAVEAETIAAYNGESSGWGTGHDEV  VQVGDEEEEIPARVNYDTTVDTFIGVNCEVATETATQGHATEGGKXYDTPSTGTQTGDYG ASQTIKSTTKRSPKPPNKKKTKKVIESEEITEVKDNKKNRTKKFTFK		223 227 347 YDVEETTYVTEESTYAPTKSETNAPTERMHYAHIEKPCDTEVTMYAPTEETT 406 228SKETSLTVAPTETTYE-TKETT-TTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTS 282 407 XAPTEETTYAPTEETTYTPTEETTYAPTEETTYAPTEETTYAPTEETT 451 283 KVLAKPTPKAETTTKGPALTTPKEPTPTT	TTPK ETPY KEPT YAPT TPKE	455 PAPTTPKEPAPTTTKEPSPTTPKEPAPT-TTKSAPTTTKEP- 494  [

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R; Leimbach, D.  submitted to the EMBL Data Library, January 1996 A; Description: The sequence of C. elegans cosmid F35A5. A; Reference number: 218485 A; Accession: T16251 A; Actuals: preliminary; translated from GB/EMBL/DDBJ A; Residues: 1-1274 < LEI>A; Residues: 1-1274 < LEI>A; Residues: 1-1274 < LEI>A; Residues: UNIPROT: Q20007; EMBL: U46675; NID: g1166613; PID: g1166621; PIDN: AABB526 A; Experimental source: strain Bristol N2; clone F35A5 C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics:	RSPKEPNKKKTKK RAPPTPIKNPAKKKRPPWES SGLDNGDFKYTTPDTSTTQ  TVETKETTTTNKQTSTDGK  TVETKETTTTNKQTSTDGK  TVETKETTTTNKQTSTDGK  TVETKETTTTNKQTSTDGK  TVETKETTTTNKGTSTDGK  TVETKETTTTNKGTSTDGK  TVETKEPTTTNKGTSTDGK	PSPTTPKEPAPTTTKSA

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3645	GSHTLVIKDTNNADFGKYTCQATNKAGKDETVGELKIPKYSFEKQTAEEVKPLFIEPLKE 3704	
1153	DIVFTRCNCEGKTFFFKDSQYWRF	
3705	TFAVEGDTVVLECKVNKESHPQIKFFKNDQPVEIGQHMQLEVLEDGNIKLTIQNAKKEDV 3764	
1177	TN-DIKDAGY 1185	
3765	GAYRCEAVNVAGKANTNADLKIQFAAKVEEHVTDESGQLEEIGQFETVGDTASSKTDTGR 3824	
1186	PKPIFKGFGGLT 1197	· · ·
3825	GAPEFVELLRSCTVTBKQQAILKCKVKGEPRPKIKWTKEGKEVEMSARVRAEHKDDGTLT 3884	
1198		
3885	LTFDNVTQADAGEYRCEAENEYGSAMTEGPIVTLEGAPKIDGEAPDFLQPVKPAVVTVG 3944	
1208	KYKNWPE-SVYFFKRGGSIQ	
3945	ETAVLEGKISGKPKPSVKWYKNGEELKPSDRVKIENLDDGTQRLTVTNAKLDDMDEYRCE 4004	
1229	IYKQEPVQKCPGRRPAL	
4005	ASNEFGDVWSDVTLTVKEPAQVAPGFFKELSAIQVKETETAKFECKVSGTKP 4056	
1265		
4057	DVKWFKDGTPLKEDKRVHFESTDDGTQRLVİEDSKTDDQGNYRİEVSNDAĞVAN 4110	

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NAlternate namers extracallular glucoamylase; mucin-like protein MCC1, protein NALtate namers extracallular glucoamylase; mucin-like protein MCC1, protein NALtate namers extracallular glucoamylase; mucin-like protein MCC1, protein NALtate namers extracallular glucoamylase; mucin-like protein MCC1, protein NALtates States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States States S 1345 1320 1329 4350 4351 IPDAKTKDNGDGSYSLEIPNAQVEDAADYKVVVSNDAGDADSSAALTVKLADDGKDKVKP 4410 --VTSA---- 1310 | | | | | : : | 4171 VQVTESEYKLEIESAEMSDTGAYRVVLSTDSFSVESSATVTVTKAAEKISLPSFKKGLAD 4230 ::| ::: | | | : | | : | | : | | : | | : | | : | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 4231 QSVPKGTPLVLEVEIEGKPKDVKWYKNGDEIKDGKVEDLGNGKYRLTIPDFQEKDVGEYS ---GYDYYAFSK-4291 VTAANEAGEIESKAKVNVSAKPEIVSGLVPTTVKQGETATFNVKVKGPVKGVKWYKNGKE --ISLPNIRK--SRTARAI------TTRSGQTLS---KV------WY 1358 ---DQYYNIDVP-------LWRGLPNV 1292 NEVKVSI--1346 1319 1330 1311 1321 В ð g à 셤 à qq à g ò

A;Map position: 9R C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase

A,Gene: SGD:MUC1, STA2, NAL5; DEX2; SGD:S0001458 A,Cross-references: MIPS:XIR019c; SGD:S0001458

A;Residues: 1-1367 <LAM> A;Cross-references: GB:U30626; NID:g1304386; PIDN:AAC49609.1; PID:g1304387

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,	igination of the same	ОУ 769 STTSDKPAPTTPKETAPTTPKEPAPTT
Query Best Match	Query Match 13.3%; Score 971; DB 1; Length 1367; Best Local Similarity 22.3%; Pred. No. 7.9e-13; Matches 377; Conservative 128; Mismatches 487; Indels 700; Gans 76;	887
λŏ	SSCAGRCGEGYSRDATC4	OY 827 HKSPDESTPELSAEPTPKALENSPKEE
QQ	:  : ::       :  6 LLAYLVLSLLENSALGFPTALVPRGSSEGTSCNSIVNGCPNLDFNWHMDQQNIMQYTLDV 65	944
λ̈́O	50 49	880
Db	66 TSVSWVQDNTYQITIHVKGKENIDLKYLWSLKIIGVTGPKGTVQLYGYNENTYLIDNPTD 125	999 TSGCS
à	50	Qy 930ITTLKTTTLAPKVTI
Db		Db 1059 TFVTKNIPTTYLTTIAPTPSVTTVTNF
ζ	77 SFERGREC 90	QY 978 PQKPTKAPKKPTSTKKPKTMPRVRKPK
Db	172 SFDLSTGCNNYDNQGHSQTDFPGFYWNIDCDNNCGGTKSSTTTSSTSESSTTTSSTSESS 231	Db 1106TSGCSPKT
ò	91KKYDKCCPDYESFCAEVHNPTSPPSSKKAPPPSGASQTIK 130	Qy 1030 LQTTTRPNQTPNSKLVEVNPKSEDA
qo		Db 1140 TTIVVTTESSIGINSA-
QY	131 STIKRSPKPPNKKKTKKVIESEEITEVKDNKKNRTKKKPTPKPPVVDEAGSGL 183	QY 1088 QGIIINPMLSDETNICNGKPVDGLTTL
qq	DITPCIKKKITISKICIKKITIPVP	Db 1156
à	SPKITTAKPINPRPSLPPNSDTSKRTSLTVNKETT	Qy 1148 IPSPIDTVFTRCN
Db	:	Db 1188 VPTTITTTECSAATNAAGETTSVCS
λ̈́O	KVLAKPTPKAETT	Qy 1196 LTGQIVAALSTAKYKNWP
Db		Db 1216IVSSASAGENTAPSATTPVTTAI
oy Vo	296 TKGPALITPKEPTPTTPKEPASTTPKEPTPTTIKKSAPTTPKEPAPTT 342	Qy 1235 VQKCPGRRPALNYPVYGEMT
Db	STTESSSAPVP	Db 1272 TTLIPGSNGAKNYETVATATNPISIKT
δ	PTTPKEPAPTTTKEPAPTT	QY 1286 DKGVLHNEVKVSILWRGLPNVVTSAIS
Db		Db 1314
٥٨	403TTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTP 452	Qy 1346 TTRSGQTLSKVW 1357
Db	512 VPTPSSSTTESSSAPAPTPSSSTTESSSAPVTSSTTESSSAPVPTPSSS 560	Db 1333 ATYSVPSISSTY 1344
δy	KEPAPTTK	RESULT 11
qq	561 TIESSSTPUTSSTTESSSAPVPTPSSSTTESSSAPVPTPSSSTTESSSAPAPTPSSS 617	T42629 tenascin-X - bovine
Qy	504 TIPKEPSPITIKEPAPITPKEPAPI- IPKKPAPITPKEPAPITPKEPAPITTKKPAPITAP 562	N,Alternate names: flexilin C,Species: Bos primigenius taur
qq	618 TTESSSAPVTSSTTESSSAPVPTPSSSTTESSSAPVPTPSSSTTESSSAPVP 669	C;Date: 11-Jan-2000 #sequence_r C;Accession: T42629
λŏ	563 KEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPE 619	R,Elefteriou, F.; Exposito, J.Y J. Biol. Chem. 272, 22866-22874
qu	670 TPSSSTTESSSAPVTSSTTESSSAPVTSSTTESSSAPVPTFSSSTTES 717	A, Title: Characterization of th A, Reference number: Z22180; MUI
٥y	620 BPAPT-TPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPT-TPKGTAPT 672	A;Accession: T42629 A;Status: preliminary; translat
qq	718 SSAPVPTPSSSTTESSSAPVPTPSSSTTESSSAPVTSSTTESSSAPVPTPSSSTTE 773	A; Molecule type: mRNA A; Residues: 1-4135 <ele></ele>
δλ	673 TLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPT 725	A; Cross-references: UNIPROT:018977; EMBL: C; Genetics:
q	774 SSSAPVPTPSSSTTESSSAPVPTPSSSTTESSVAPVP-TPSSSSNITSSAPSSTFFSS 830	C; Superiamily: tenascin-X; BGF homology; Creaming C; Superiamily: tenascin-X; BGF homology;
ò		civeywords: excracellular macri

KTTESKITATITQVEST--TTQDTIPFK----- 929 | CLRNGTLVAFRGHYFWMLSPFSPARRITEVWG 1147 CECKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGG 1195 SAKT----- 1215 NETPITITITIVC-----STGINSAGET-- 1105 JAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPN 1087 -----ESVYFFKRGGSIQQYIYKQEP---- 1234 ---- OVRRRRFERAIGPSQTHTIRIOYSPARLAYQ 1285 SLPNIRKPDGYDYYAFSKDQYYNIDVPSRTARAI 1345 PKTTPTPRKMTSTMP-----ELNPTSRIAEAM 1029 aipttvittesävgtnsagetttgyttksipttyi 1271 TTPKKPAPTTPET--PPPTTSEVSTPTTTKEPTT1 826 SSTTESSVAPV----PTPSSSSNITSSAPSSIPFS 886 EPGVPTTKTPAATKPEMTT-----TAKDKTTER 879 --TKKTITTTEIMNKPEETAKPKDRATNSKATTPK 977

1-Jan-2000 #text_change 09-Jul-2004

e, R.; Lethias, C.

tenascin-X, 16; PMID:9278449

B/EMBL/DDBJ

:Y11915; NID:g2462978; PIDN:CAA72671.1; PID:g246 fibrinogen beta/gamma homology, fibronectin typ votein; heptad repeat

8 4 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6	8 8 8 8 8 8 8 8
Query Watch   12.7%;   Score 931.3;   DB 2;   Length 4135;	Db 1224 TLPGIANKNRHGPLHADGTHAPEKKEBPRHPERPLIGELTVAGAHADSIRLŚWTVAQ 1283  255TDGKEKTTSAKETQSIEKTSAKDLAPTSK
6 16 16 16 16 16 16 16 16 16 16 16 16 16	

	741TTLKEPAPTTPKK-PAPKELAPTTKGPISTISDKPAPTTPKE 782 2650 FHDRORMGPVSVIGYTTARBETPGPTAMFORDER-LAPTTREMREPRESEDENT 2706	0y 1055 G   Db 3689 GEPQSVQVDGRTQKLEG
	TAPTTPKR	QY 1096LSDETNICNGK
		Db 3741 HLRALNLTDESALLHWK
		OY 1117 -GILVAFRGHYF
	-	
	808	1138
	2827 LGDLTVTGSSPDSLSLSWTVPQGHFDSFTIQYKGRDRPQVVRVGGEETEVTIGGLEPRHK 2886	
	808 PPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEP 841	1154
	2887 YKMNLYGLHGGRRVGFVSTVGVTAPDYDAMITQTPSISVPEPPTKPRLGBVTV 2939	3921
	842TPKAL	RFTND
	2940 IDATPDSLSLSWIIPEGQFDHFLVQYKNGDGQPKAVRVPGDEDGVIISGLEPDHKYKMNL 2999	OV 1933 RDVOKCDCDDDDINADV
	GVPITKTPAATKPEMITTAKDKTTERDLRTIPETTTAAPKMIK 896	4007
	YGFHUHQKVGPVSVIGVITAEEETPSPIKMEEIPSPIEME	QY 1293 EVKVSILWRGLPNVVTS
8 AA	89/ ETATITEKITES	4024
		Qy 1349 SGOTLS
	VRVGG	Db 4055 SGSVFSARDRDPNNLLI
	94	RESULT 12
	:	S49915 extensin-like protein - maiz
	941KVITTKKIITTTEIMNKPEETAKP964	C;Species: Zea mays (maize) C;Date: 05-Mar-1995 #sequenc
	3220 LFGLRDEKRHGPVSADAKTLPDTKPAPRLGELTVTDVTPGSVGLSWTVPB 3269	C; Accession: S49915 R; Rubinstein, A.L.; Broadwat
	965KDRATN 970	submitted to the EMBL Data L A;Description: Pex genes: po
	3270 GEFDSFMVQYKDRDGQPRVVPVAADQREVTVPGLEPNRKYKFLLYGLVGRKRLGPISAEG 3329	A;Reference number: S49915 A;Accession: S49915
	971 SKATTPKPQKP 981	A;Status: preliminary A;Molecule type: DNA
	3330 STAPLEKERQPPPRLGELTVTDETPNSLRLSWTVAQGRFDSFVVQYRGTDGQPRMVPVAA 3389	A;Residues: 1-1188 <rub> A;Cross-references: UNIPROT:</rub>
	982TKAPKKP 988	Query Match 12.5%
	3390 DQREFTVEGLEPGRKYKFLLYGLLGGQRLGPASVLGMTAPEEDTPAPWHAATEAPKPPEG 3449	Best Local Similarity 18. Matches 299; Conservative
	886 686	Qy 10 LLLLLSVFVIQQVS
	3450 PRLGVLAVRDVSPDSLRLSWSVVQGPFDSFVVQYQDTDGQPQALLVGGDQNKVLVSGLEP 3509	Db 17 LLLLAACLSACSVQAVTS
	886 686	9y 37
	3510 STSYEFFLYGLHEGKRLGPVSAEGTTGPVPAGQTPGEPGPRLSHLSVTDVTTSSLRLNWE 3569	Db 77 PRLRRAYIALQAWHRAF
	9891STKKPKTMPRVRKPKTTPTPTRATSTMPELNP 1021	Oy 69 SCKGR
	3570 APPEAFDSFLIRFGVPSPSTLEPQLRPLLQRELTVPGTRR-SAVLRDLHPGTLYTLTLYG 3628	Db 133 DINGADIAGYLPPELGL
0y 10	1022TSRIABAMLQTTTRPNQTPNSKLVEVNPKSEDA 1054	Oy 74CFES
	3629 LRGPHKADSIQGTARTLSPVLESPRDLOPSBIRETSARVSWTPPTSRVDGFKVSYOLADG 3689	Db 193 VVCI.EMVSI.KVI.DI.BENI

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ογ	60	עכ	80
QQ.	249	VIVFANNAFVGCIPKSIGRMVKTLDEIIFLNNKLDGCLPLEMGLLVNTTVIDVSGNMLVG 3(	808
δλ	66	11	111
qq	309	TIPEQLSNIAKLEQLDVSRNVFTGIVHESICELPALVNFSFAFNFFNSEAAVCMFSDKAL 36	368
ζζ	112	SPPSSKK 11	118
qq	369	VNLDDRDNCLGALRPAQKTALQCAPVLARPVDCSKHVCAGYPTPGGGPPSSPVPGKPAAS 42	428
QY	119	TIKSTTKRSPKPPNKKKTKKVIESEEITEVKDNKKNRTKKKPTPKPPVVDE	178
qa	429		468
٥٧	179	KVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKE	238
Dp	469		503
55	239	TTVETKETTTTINKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKG 20	298
Db	504	VKLSPPQAPVGSPPPVKTTSPP 5	526
ογ	299	PALITIPKEPTPTTKEPTPTT 33	327
qq	527	APIGSPSPPPPVSPPPPVKSPPPPPAPVGSPPPPBKSPPPPAPVASPPPPVKSPPPPT 50	586
δy	328	ω-	384
ηp	587	LVASPPPPAKSPPPPARSPPPTPVASPPPPARASPPPARSPPPARSSPPPMKSPPPTPVS 6	646
٥٧	385		434
Db	647	SPPPPEKSPPPPPAKSTPPPEEYPTPPTSVKSSPPPEKSLPPPTLIPSPPDGEKPTPPS 71	706
δ,	435	TTTKEPSPTTPKBPAPTTTKSAPTTT	491
qu	707	TPSKP-PSSPEKPSPPAPVSSPPALA 71	756
δy	492	KEPAPITIKSAPITPKEPSPITIKEPAPITIPKEPAPITPKKPAPITPKEPAP 5	551
Db	757	- _Д	811
ζŏ	552	TITKKPAPTAPKEPAPTTPKETAPTIPKKLTPTTPEKLAPTTPEKPAP 5	599
Db	812	OVEKTSPPRAPLSSPPLAPKSSPPHVVVSSPPPVVKSSPPRAPVSSPPLTPKPASPPAHV 8	871
٥y	009	EEPTPTTPEEPAPTTPKAAAPNTPKE-PAPTTPKEPAPTTPKEPAPTT	657
Db	872		927
ζ	658	ω-	703
QC	928	PKSSPPPVVVSSPPPTVKSSPPAPAPKSSPPAPKASPPPAPVNLPPPEVKSSPPPTVSS 9	987
δχ	704	PITPKGTAPTTP-KEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPT	762
Db	988	PPPAPMSSPPPEVKSPPPAPVSSPPPVKSPPPPAPVSSPPP	1039
٥y	763	TIKGPISITSDKPAPITPKETAPITPKEPAPITPKKPAPITPETPPPITSEVSTPITKE 8	822
Db	1040	PVKSPPPPAPVSSPPPPVKSPPPPAPISSPPPPVKSPPPPAPVSSPPPPVKS 1	1091
ζ	823	PITIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTITAKDKTTERDLR 8	882
QQ	1092	P	1095
δy	883	TTPETTTAAPKWIKETATTTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKV 9	942
Dp	1096	1	1095

λŏ	943	TTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRK 1002
qq	1096	
ò	1003	PKTTPTPRKMISTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETP 1062
qq	1124	PPSLPPPAPVSSPPPVVTPAP1151
δλ	1063	HMLLRPHVFMPEVTPDMDYLFRVPNQGIINPMLSDETNICNGKPVDGLTTLRNGTLVAF 1122
οp	1152	
δλ	1123	RGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDI 1180
qa	1154	11PPAESQPPPSFNDIIL 1169
οχ	1181	KDAGYPKPIFKGF 1193
Dp	1170	PPIMANKYASPPPPQF(
RESULT A41819 proline C; Specie C; Date:	13 -rich E es: Rat 13-May	RESULT 13 A41819 proline-rich peptides 637K precursor, prostatic - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 09-Jul-2004
C; Acces R; De Cl J. Biol	sion:   ercq,   Chem	A42663; A41819; A31966; B20593; A20593 N.; Hemachoote, K.; Devos, A.; Peeters, B.; Heyns, W.; Rombauts, W. . 267, 9884-9894, 1992 4 4-kilodalton proline-rich polypeptides of the rat ventral prostate are tl
le exon A;Refer	ence n	1577819
A; Molec	sion: Jule type	442663 9-20 DNA; mRNA 9-20 - 11 3-00 ADD 15 ADD 4155 /S/ 4157-5761 ADD 2
A; Kesid A; Cross A: Exper	refer refer imental	אחר זפור-ופדני פ
A, Note:	seques	le translation NCBIN:100347, NCBIP:100348)
R,De Cl submitt	ercq, 1 ed to 1	N.; Hemschoote, K.; Devos, A.; Peeters, B.; Heyns, W.; Rombauts, W. the Protein Sequence Database, April 1992
A; Refer A; Acces	ence n	umber: A41819 A41819
A; Statu A; Molec	s: not	compared with conceptual translation pe: DNA
A;Resid R;Hemsc	ues: 1 hoote,	-5762 <de1> K.; Peeters, B.; Dirckx, L.; Claessens, F.; De Clercq, N.; Heyns, W.; Win</de1>
J. Biol	. Chem : A si	. 263, 19159-19165, 1988 ngle 12.5-kilobase androgen-regulated mRNA encoding multiple proline-rich
A;Reter A;Acces	sion:	MINDET: ASI966; MULD:89066/ZL; FMID:319861/ 
A; Molec A; Resid	ule ty. ues: 3	THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF TH
A;Cross R;Peete	-reier rs, B.	20659// FIDN:AMALISSO.I, FID:GSSTR.
J. Biol A;Title	. Chem : Prol.	. 258, 14206-14211, 1983 ine-rich polypeptides bound to rat prostatic binding protein. The primary
A;Refer A;Acces	ence n	PMI
A, Molec	ule tyn	
A; Note:	this	peptide, designated proline-rich polypeptide V, can be found at several lo A20593
A, Molec A, Resid	ule tyn	111
A;Note: C;Genet	cnis ics:	on polypeptide iv, can be found as several
A; Intro A;Note: C;Super	ns: #s singl family	tarus absent e copy gene with no introns : rat prostatic proline-rich peptides 637K precursor
C; Keywo F;1-26/	rds: p	rostate; tandem repeat : signal sequence #status predicted <sig></sig>
F;27-57	61/Pro	eptides 63/A proprocein #scacus predicted

CAGRCGEGYSRDATCNCDYNCOHYMBCCPDFKRVCTAELSCKGRCFEPSHLKTSTLSKPPVVSNTKSSAFOETWST PIDSTGGG
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October 13, 2004, 11:23:49; Search time 105.696 Seconds (without alignments) 4449.477 Million cell updates/sec

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SEQ1-H 7064 Perfect score: Sequence:

1 MAWKTLPIYLLLLLSVFVIQ......ARAITTRSGQTLSKVWYNCP 1311

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.1

Searched:

2002273 Total number of hits satisfying chosen parameters:

2002273 seqs, 358729299 residues

Minimum DB Maximum DB

seq length: 0 seq length: 200000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

23Sep04:* Database

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SUMMARIES

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## ALIGNMENTS

Human; extracellular messenger; EXMDS; respiratory-gen.; antiallergic; antialsthmatic; antiinflammatory; antidiabetic; neuroprotective; muscular-gen.; antiarthritic; osteopathic; hepatotropic; antipsoriatic; virucide; fungicide; antiparasitic; protozoacide; antihelminthic; cytostatic; gene therapy. Human extracellular messenger (EXMES) polypeptide. ADK67912 standard; protein; 1311 AA. (first entry) Homo sapiens, 06-MAY-2004 ADK67912; RESULT 1 ADK67912 

Location/Qualifiers Peptide

or 30 29 24, 21, 1. .30
/label Signal_peptide
/note= "Spans residues 1 to 18, 20,
according to identification method"

WO2004013292-A2

12-FEB-2004

30-JUL-2003; 2003WO-US024084.

2002US-0400810P. 2002US-0412197P. 2002US-0416004P. 02-AUG-2002; 2 19-SEP-2002; 2 04-OCT-2002; 2

08-NOV-2002; 2002US-0424862P

(INCY-) INCYTE CORP.

Elliott VS, Khare R, Tran UK, Swarnakar A, Marquis JP; Richardson TW, Emerling BM, Lindquist EA, Chawla NK, Ramkumar J; Lee SY;

WPI; 2004-157116/15. N-PSDB; ADK67917. New extracellular messengers and nucleic acids, useful for diagnosing, treating or preventing e.g. allergies, anemia, Crohn's disease, diabetes mellitus, myasthenia gravis, osteoporosis, psoriasis, cancers or autoimmune thyroiditis.

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The present sequence is that of novel human extracellular messenger

(EXMES) Incyte ID NO: 7513018CD1 polypeptide. The protein shows homology

(EXMES) Incyte ID NO: 7513018CD1 polypeptide. The protein shows homology

(C) to human megakaryocyte stimulating factor. The invention provides EXMES

(C) polynucleotides and polypeptides, as well as expression vectors, host

(C) creating or preventing disorders associated with aberrant expression of

(C) EXMES, especially autoimmune and inflammatory disorders, cell

(C) EXMES, especially autoimmune and inflammatory disorders, cell

(C) EXMES, especially autoimmune and inflammatory disorders, cell

(C) EXMES, especially autoimmune and inflammatory disorders, cell

(C) distress syndrome, allergy, anaemia, erythroblastosis foctails, Crohn's

(C) distress syndrome, allergy, anaemia, erythroblastosis foctails,

(C) ciscoporosis, pancreatitis, psoriasis, viral, bacterial, fungal,

(C) parasitic, protozoal or helminthic infections, cancers, autoimmune

(C) parasitic, cretinism, Plummer's disease or thyroid carcinoma.

(C) Exmes, including determining of efficacy, dosage, toxicity and

(C) pharmacology, and for investigating the pathogenesis of diseases and

(C) medical conditions.
SEQ ID NO 5, 165pp; English.
                  Claim 60;
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Sequence 1311 AA;

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tch (al Similarity 99.9%; Score 7058; DB 8; Length 1311; (al Similarity 99.3%; Pred. No. 3.4e-171; 1310; Conservative 0; Mismatches 1; Indels 0; Gaps	MAWKILPIYLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF	MAWKTLPIYLLILLISVEVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF		KRÝCTABLSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVKDNKKNRTKKKPT	PKPPVVDBAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKE		TSLIVNKETTVETKETTTINKQISIDGKEKITSAKETQSIEKTSAKDLAPISKVLAKPIP	-⊢	. KAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTTSAPTTPKEPAPTTTKSAPTTP		KEPAPITIKEPAPITIPKEPAPITITKEPAPITIKSAPITIKSAPITIPKEPAPITIPKEPAPITIPKEPAPI		TIPKEPIPTIPKEPAPTIKEPAPTIPKEPAPTAPKKPAPTIPKEPAPTIPKEPAPTITKE	TIPKEPIPTIPKEPAPTIKEPAPTIPKEPAPTAPKKPAPTIPKEPAPTIPKEPAPTITKE	1 PSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPAPTTPKEPAPTTP	1 PSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKBPAPTTPKEPAPTT	1 KKPAPITPKEPAPITPKEPAPITTKKPAPTAPKEPAPTTPKETAPTTPKKLTPFKLM	-		PT-	KEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTKEPT		1 PKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTST
Query Match Best Local : Matches 131	1	1	61	61	121	121	181	181	241	241	301	301	361	361	421	421	481	481	541	541	109	601	661
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66121 abel= Ex 13126 abel= Ex	/label= Exon X  13311373  /label= Exon X	3731404	tiii label=			92WO-US000433.	91US-00643502. 91US-00757022.	CS INST INC.	ark SC, Jacobs K, He	60/34. 23.	-karyocyte stimulati cancer, exposure to c.	3; Fig 1; 87pp; Eng	74 0	addition of an lating methionin	exon IV. The cDNA	the initiating met n secretion signal	includes exons II	different MSF	activity of the fac ling and processing	V - XII are b	e appiopilate st exons may conta on: organisation	on, organization of g. Both naturally racterised by wari	his sequence, form differen	rrect PN field	AA;
Region Region	Regi	Region		WO9213075-A1.	06-AUG-1992.	17-JAN-1992;	18-JAN-1991; 10-SEP-1991;	(GEMY ) GENETI	Turner K, Cla	WPI; 1992-2846 N-PSDB; AAQ272	New human mega- deficiencies, d infections, etc	Claim 1, 2 and	g H e	- °	n followi	conta in pr	nai meg on betwe	h encoding	ability, pught to	ss. Exo	more of the	trix proces F's may be	liced exons	-MAR-2003 to	Sequence 1404
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cancer, exposure to radiation or drugs, bacterial and viral for treating immune ocyte stimulating factors infections, etc. deficiencies,

Gesner IG;

Hewick RM,

Claim 1, 2 and 3; Fig 1; 87pp; English.

The sequence given is a full length translation from the megakaryocyte stimulating factor (MSF) precursor. The sequence covered by exons II, III and I be encodeds megakaryocyte stimulating factor (MSF). This sequence is modified by the addition of an N-terminal sequence encoding a secretory codon following exon IV. The cDMA sequence given contains a sequences of codon following exon IV. The cDMA sequence given contains sequences of codon following exon IV. The cDMA sequence given contains sequences from I contains the initiating methionine, and encodes a classical exon I contains the initiating methionine, and encodes a classical corriginal meg-GSF includes exons II-IV and is thought to terminate in the region between amino acid residues 134 - 147. The primary transcript of this gene may be cleaved in different ways to yield a family of mRNA's cach encoding a different MSF protein. Exons V and VI are thought to be each encoding and inferent MSF protein. Exons V and VI are thought to be stability, folding and processing of the molecule. These exons are also chought to play a role in the observed synesyp of MSF with other cytokines. Exons V - XII are believed to be implicated in the processing or folding of the appropriate structure of the resulting factor, ie. one contain sequences which direct proteolylical contains sequences which direct proteolylical contains expensed to be implicated in the processing or more of these exons may contain sequences which direct proteolylical contains expensed to be implicated in the processing of manner and an expense exone may contain sequences which direct proteolylical contains expensed to be implied to the contains expense exone and the contains expense exone exception of the lange exone may contain sequences which direct proteolylical expenses exone exceptions. cleavage, adhesion, organisation of the cellular matrix or extracellular matrix processing. Both naturally occuring and non-naturally occuring MSF's may be characterised by various combinations of alternatively spliced exons from this sequence, with the exons spliced together in differing orders to form different members of the MSF family. (Updated on 25-MAR-2003 to correct PN field.)

106 09 9 MAWKTLPIYLLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF Gaps 93; 99.7%; Score 7044.7; DB 2; Length 1404; 93.4%; Pred. No. 8.2e-171; oi. Mismatches 0; Indels 93; KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAE-Conservative Similarity Matches 1311; Н ч Query Match 61 g ð ò

KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP 120 147 1047 207 267 360 447 540 1080 300 327 420 387 507 009 567 099 1020 1048 DETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPARRITEVWGIPSPIDTVFT 1107 627 720 687 927 987 780 747 840 900 867 096 807 121 PPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEEHSVSENQESSSSSSSSSSSTIW TQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTNKQTSTDG ----VKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTST 181 KIKSSKNSAANRELQKKLKVKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTST KEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPAS **APTITIKSAPTIPKEPAPTIPKKPAPTIPKEPAPTIPKEPTIPKEPAPTIKEPAPTIKEPAPTIPK** TTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEP **EPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPT** TIKSAPTIPKEPSPITIKEPAPTIPKEPAPTIPKKPAPITPKEPAPITIKKP 541 TTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKP 508 APTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTT 601 APTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTTT 568 PEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEP APTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKG TAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPK PQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPN POKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPN **QTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLS** KPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPT TKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKLTATTTQV TKTPAATKPEMTTAKDKTTERDLRITPETTTAAPKMTKETATTTEKTTATTAGV TSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPK 148 241 208 301 268 361 421 448 107 107 328 388 628 721 688 781 841 901 196 748 808 868 928 1021 1141 988 ò g à 염 ò g ò Db à dd ò g à g à 셤 à g à g  $\delta$ 셤 ò g ò g  $\delta$ g à g ò g qq ð ò

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The invention relates to a human tribonectin which is a product of alternative splicing of the human MSF (megakaryocyte stimulating factor) calternative splicing of the human MSF (megakaryocyte stimulating factor) gene. The tribonectin has at least one 0-linked oligosaccharide lubricating moiety and has a polypeptide sequence comprising 1-76 repeats of a motif having at least 50% identity to the sequence KEPAFTT of ABASPTA). The invention also relates to a mucleic acid encoding a human MSF-derived tribonectin; a biocompatible composition comprising a human tribonectin for inhibiting tissue adhesion formation; and a method of tribonectin of MSF or its fragment in a biological sample of a mammal, wherein an increased amount of MSF compared to a control mammal, wherein and DNA encoding it are useful in the treatment of the tribonectin and DNA encoding it are useful in the treatment of such as articulating joints of humans, dogs or horses. The tribonectin, when formulated as a membrane, foam, gel or fibre, is useful for inhibiting adhesion between two surfaces such as the injured tissues of a mammal, where the injury is caused by a surgical insertion or trauma, or
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                                                                                                                                                     SPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYYAFSKDQYYNIDV
                   RCNCEGKTFFFKDSQYWRFTND1KDAGYPKP1FKGFGGLTGQ1VAALSTAKYKNWPESVY
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an artificial device e.g., an orthopaedic implant. In particular, one the surfaces is pericardial tissue. DNA encoding a tribonectin may be used in gene therapy. The present sequence represents human MSF
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                                                                                                                                                                                 KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAE-
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                                                                           Score 7044.7; DB 4;
pred. No. 8.2e-171;
0; Mismatches 0;
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Best Local Similarity 93.4%;
Matches 1311; Conservative
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TSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPK
                                 PQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIABAMLQTTTRPN
                                                                                Human, CACP protein, camptodactyly-arthropathy-coxa vara-pericarditis,
MSF; megakaryocyte stimulating factor; synovial lubricant;
chromosome 1q25-31; osteoarthritis; joint lubrication; osteopathic;
                                                                                                      DETNICHGKRVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFT
                                                                                                                  RCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVY
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The invention relates to a method of treating osteoarthritis via the

Example 1; Page; 34pp; English

New composition comprising the camptodactyly-arthropathy-coxa varapericarditis protein in combination with an anesthetic, useful for treating osteoarthritis, or as lubricants of tissue and joints.

CASE WESTERN RESERVE.

(UYCA-) UNIV

Warman ML;

WPI; 2001-182721/18.

administration of a composition comprising the camptodactyly-arthropathycoxa vara-pericarditis (CACP) protein, or portions of the CACP protein.

The composition may further comprise a local annestheric. The composition of the invention may be administered via intra-articular or intravenous injection. The human CACP protein is identified in the invention as being CC megakaryozyte stimulating factor (MSF). The game encoding CACP protein (MSF) is located on chromosome 1q20-31, and mutations in this gene are responsible for the heritable disorder camptodactyly- arthropathy-coxa vara-pericarditis, in which patients have synovial hyperplasia without cerificant, and can be used to lubricate tissue and joints in the special conferont of osteoarthritis. The composition may be applied to reduce the symptoms of osteoarthritis (e.g., joint pain, loss of range of movement or joint damage). The present sequence represents human megakaryocyte stimulating factor (MSF, CACP protein). Note: This sequence is not given in its entirety in figure 4 of the specification, although a GenBank accession number was given. This sequence obtained from 106 180 147 240 207 300 267 360 327 420 9 9 387 480 447 540 507 009 267 099 PEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEP 627 720 121 PPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEEHSVSENQESSSSSSSSSSSTIW 1 MAWKTLPIYLLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF TQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDG KEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPAS 181 KIKSSKNSAANRELQKKLKVKDNKKORTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTST -------VKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTST KEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPAS TTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEP **APTITKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTTPKEPAPTTKEPAPTTPK** APTITKSAPITPKEPAPITPKKPAPITPKEPAPITPKEPIPKEPAPITFKEPAPITKEPAPITKEPAPITF **EPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTKSAPTTTKEPAPT** BAPTAPKKPAPTTFKEPAPTTPKEPAPTTTKEPSPTTPKEPAPT TTKSAPTTPKEPSPTTTKEPAPTTPKKPAPTTPKKPAPTTPKEPAPTTTKKP APTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTT Length 1404; 93; Indels KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAE 4; Score 7044.7; DB 4; Pred. No. 8.2e-171; 0; Mismatches 0; 99.78; Best Local Similarity 93.4 Matches 1311; Conservative Sequence 1404 AA; 61 61 Query Match 107 107 148 208 301 328 421 268 361 388 481 448 541 508 199 268 ò g DP à ò d g  $\overset{\circ}{\circ}$ à ద ò qq δ 셤 δ g g à Š g q à ò

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New tribonectin polypeptides and polymucleotides for lubricating joints or other tissues to prevent or treat Camptodactyl-arthropathypericarditis syndrome or osteoarthritis.
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                                                                                                                                                                                                                                                                        lubricating polypeptide; O-linked oligosaccharide; joint lubrication; CAP; camprodactyl-arthropathy pericarditis; osteoarthritis; human; megakaryocyte stimulating factor; MSF.
                                                                                                                                                TSTTIQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPK
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          TAPITLKEPAPITPKKPAPKELAPITIKGPISITSDKPAPITPKETAPTTPKEPAPITPK
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                   The invention relates to a lubricating polypeptide and at least one O-linked oligosaccharide. The composition and methods are useful for lubricating joints or other tissues to prevent or treat camptodactylarthropathy perioarditis (CAP) or osteoarthritis in mammals. The present sequence represents the amino acid sequence of the human megakaryocyte stimulating factor (MSF).
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.larity 93.4%; Pred. No. 8.2e-171;
Conservative 0; Mismatches 0;
English
1; SEQ ID NO 1; 34pp;
                                                                                                                                                                                   Best Local Similarity
Matches 1311; Conser
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                                                                                                                Human, vaccination, gene therapy, nutritional supplement;
stem cell proliferation, haematopoiesis, nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                       Novel human secreted protein #2753.
                                                                                                                                                                                                                                                              16-APR-2001; 2001WO-US008656
                                                             (first entry)
                                                                                                                                                                                                     WO200179449-A2
                                                            18-DEC-2001
                                                                                                                                                                                                                               25-OCT-2001
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492

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The invention relates to novel human secreted polypeptides. The polypeptides are useful for determining the presence of or predisposition to a disease associated determining the presence of or predisposition to a disease associated with alreard levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapoutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis, and in bone, cartilage, tendon stimulation; as anti-inflammanchy agents; and in treatment of leukaemias. ANU29510-AAU33304 represent the amino acid sequences of novel human
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                                                                                                                                     Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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Pred. No. 9.9e-171;
L; Mismatches 0;
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2000US-00552929.
2001US-00770160.
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                                                                                                        WPI; 2001-611725/70
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Rest Local Similarity
                                           (HYSE-) HYSEQ INC
                                                                           Liu C,
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18-APR-2000;
                26-JAN-2001;
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Matches 1310;
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angiogenesis inhibitor; angiogenesis stimulator; angiogenic index; gene expression; cancer; coronary artery disease; myocardial ischemia; coronary arteriosclerosis; forensic medicine.

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Determining the angiogenic index of a tissue or cell sample using expression levels of differentially expressed genes, useful for diagnosing or treating cancer, coronary artery disease, myocardial

ID NO 78; 296pp; English

Disclosure; SEQ

ischemia and/or arteriosclerosis.

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Jay

Fan W,

Kovacs KF,

Li X,

Sun Z,

WPI; 2003-731502/69.

07-FEB-2002; 2002US-00067482. 10-JUN-2002; 2002US-00164595. 16-AUG-2002; 2002US-0403649P. 03-JAN-2003; 2003US-0437746P.

07-FEB-2003; 2003WO-US003848

WO2003066831-A2.

14-AUG-2003

gapiens

Homo

(ORIG-) ORIGENE TECHNOLOGIES

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360
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                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of determining the angiogenic index of a tissue or cell sample comprising assessing, in a sample, the expression levels of one or more differentially-expressed gene from any of 34 DNA sequences, given in the specification, where the levels are indicative of the angiogenic index. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating cancer, coronary artery disease, myocardial ischemia or coronary artery areas they can also be used in research, drug discovery and forensic medicine involving angiogenesis. This sequence corresponds to one of the differentially expressed proteins of the invention.
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Matches 1308; Conserv
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cytostatic; cardiant; vasotropic; antiarteriosclerotic; Angiogenesis-differentially expressed protein #53

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standard; protein; 1404

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Human, extracellular messenger; EXMES; respiratory-gen., antiallergic; antiasthmatic; antiinflammatory; antidiabetic; neuroprotective; muscular-gen.; antiarthritic; osteopathic; hepatotropic; antipsoriatic; virucide; fungicide; antiparasitic; protozoacide; antihelminthic;
                               Human extracellular messenger (EXMES) polypeptide.
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                                                                                       Location/Qualifiers
ADK67911 standard; protein; 1270
                     (first entry)
                                                                 cytostatic; gene therapy.
                                                                           Homo sapiens.
                     06-MAY-2004
          ADK67911;
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24, 21, /note= "Spans residues 1 to 18, 20, according to identification method" 1. .29 /label= Signal_peptide Tran UP ng BM, 30-JUL-2003; 2003WO-US024084. 02-AUG-2002; 2002US-0400810P. 19-88P-2002; 2002US-0412197P. 04-0CT-2002; 2002US-0416004P. 08-NOV-2002; 2002US-0424862P. Khare R, (INCY-) INCYTE CORP WO2004013292-A2 VS, 12-FEB-2004 Elliott Peptide

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or

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UK, Swarnakar A, Marquis JP; , Lindquist EA, Chawla NK, Ramkumar Richardson TW, Emerling Lee SY;

2004-157116/15. N-PSDB; ADK67916. New extracellular messengers and nucleic acids, useful for diagnosing, tracting or preventing e.g. allergies, anemia, Crohn's disease, diabetes mellitus, myasthenia gravis, osteoporosis, psoriasis, cancers or autoimmune thyroiditis.

Claim 59; SEQ ID NO 4; 165pp; English.

The present sequence is that of novel human extracellular messenger
(EXMES) Incyte ID NO: 7513017CD1 polypeptide. The protein shows homology
to human megakaryocyte stimulating factor. The invention provides EXMES
polymucleotides and polypeptides, as well as expression vectors, host
cells, antibodies, agonists and antagonists, and methods for diagnosing,
treating or preventing disorders associated with aberrant expression of
EXMES, especially autoimmune and inflammatory disorders, cell
proliferative disorders and endocrine disorders, e.g. adult respiratory
distress syndrome, allergy, anaemia, erythroblastosis foetalis,
clistass, diabetes mellitus, myasthenia gravis, osteoarthriis,
osteoporosis, pancreatitis, psoriasis, viral, bacterial, fungal,
parasitic, protozoal or helminthic infections, cancers, autoimmune
thyroiditis, cretinism, Plummer's disease or thyroid carcinoma.
Chyroiditis, cretinism, Plummer's disease or thyroid carcinoma
their encoding polymucleotides for using the purified EXMESs and/or
their encoding polymucleotides for facilitating the drug discovery
process, including determining of efficacy, dosage, toxicity and
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Sequence 1270 AA;

Gaps Length 1270; 41; Indels Score 6793.9; DB 8; Pred. No. 1.7e-164; 0; Mismatches 1; 96.2%; Best Local Similaricy Matches 1269; Conservative Query Match

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                                    KRVCTABLSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVKDNKKNRTKKKPT
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The invention relates to a method of determining the anglogenic index of a tissue or cell sample comprising assessing, in a sample, the expression levels of one or more differentially-expressed gene from any of 34 DNA sequences, given in the specification, where the levels are indicative of the anglogenic index. The methods and compositions of the present invention are useful for diagnosing preventing and/or treating cancer, coronary artery disease, myocardial ischemia or coronary artery disease, myocardial ischemia or coronary artery disease, mocardial ischemia or coronary artery disease, myocardial ischemia or coronary forensic medicine involving angiogenesis. This sequence corresponds to one of the differentially expressed proteins of the invention.
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                                                                                                                                                          GEMTQVRRRRFERAIGPSQTHTIRIQYSPARLAYQDKGVLHNEVKVSILWRGLPNVVTSA
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; 2002US-00164595.
; 2002US-0403649P.
; 2003US-0437746P.
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10-JUN-2002;
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Length 1320;

7; DB

Score 6769.9;

95.88;

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The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTE from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 1198-1201; 1275pp; English.
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A, Zhang J
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antibodies and research use.
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7, Drmanac RA,
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                           MAWKTLPIYLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF
                                                                                                 -----EVKDNKKNRTKKKPTPKPPVVDEAG
                                                                                                                                  SGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETT
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                                                                                                                                                                                                                                                                                                                                             Human, sheep, pig, cow; fruit fly; yeast; hamster; macaque; horse;
tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
diagnostics; forenaic test; gene mapping; genetic disorder; blodiversity;
                                            YLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPAR
                                                                             1040 YLPRVPNQGIIINPMLSDBTNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPAR
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                                                                                                                                                                 RITEVWGIPSPIDIVFTRCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLIGQI
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an T;
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J, Werhm
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17-JUL-2000; 2000US-00617746.
03-AUG-2000; 2000US-00631451.
15-SEP-2000; 2000US-00663870.
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tags (ESTs)

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The invention relates to a human tribonectin which is a product of alternative splicing of the human MSF (megakaryocyte stimulating factor) calternative splicing of the human MSF (megakaryocyte stimulating factor) can the tribonectin has at least one 0-linked oligosaccharide comprising in the tribonectin an polypeptide sequence comprising 1-76 repeats of a motif harving at least 50% identity to the sequence KEPAPTT of ARAB2974). The invention also relates to a nucleic acid encoding a human MSF-derived tribonectin; a biocompatible composition comprising a human tribonectin for inhibiting tissue adhesion formation; and a method of tribonectin for inhibiting tissue adhesion formation; and a method of diagnosing osteoarthritis by measuring the amount of MSF or its fragment in a biological sample of a mammal, wherein an increased amount of MSF compared to a control manual, wherein an increased amount of MSF compared to a control relationectin and DNA encoding it are useful in the treatment of The tribonectin and DNA encoding it are useful in the treatment of such as articulating joints of humans, dogs or horses. The tribonectin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human tribonectin; MSF; megakaryocyte stimulating factor; alternative splicing; joint boundary lubricant; 0-linked oligosaccharide; osteoarthritis; tribosupplementation; tissue adhesion inhibition; friction coefficient reduction; gene therapy; antiarthritic; osteopathic.
                                                                                                                                                                                1141 DETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDIVFT
                                                                                                                                                                                                                                             1048 DETNICHGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFT
                                                                                                                                                                                                                    1108 RCNCEGKTFFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVY
POKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPN
                                                                        QTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel tribonectin polypeptide useful as lubricant for treating osteoarthritis, comprises O-linked lubricating moiety.
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                                                                                                                                                                                                                                                                                            FFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGE
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                                                                                                                             1 MAWKTLPIYLLILLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF
                                                                                                                                                                                               61 KRUCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP
                                                                                                                                                                                                                                                                                  121 PPSGASQTIKSTIKRSPKPPNKKKIKKVIESEEITEEHSVSENQESSSSSSSSSSTIW
                                                                                                  1 MAWKTLPIYLLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF
                                                                    Gaps
                                                                  93;
                            4; Length 1299;
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                        Score 6468.7; DB 4
Pred. No. 3.3e-156;
0; Mismatches 0;
                              Query Match 91.6%;
Best Local Similarity 92.8%;
Matches 1202; Conservative
AA;
Sequence 1299
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  when formulated as a membrane, foam, gel or fibre, is useful for inhibiting adhesion between two surfaces such as the injured tissues of amammal, where the injury is caused by a surgical insertion or trauma, or an artificial device e.g., an orthopaedic implant. In particular, one of the surfaces is pericardial tissue DNA encoding a tribonectin may be used in gene therapy. The present sequence represents a substantial portion of a human MSF-derived tribonectin
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                                                                                                                             Length
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Pred. No. 3.2e-82;
7; Mismatches 76;
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TLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDIVFTRCNCEGKTFFFKDSQ 1122 This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention ; 0 120 623 9 οĘ DAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLT TKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEP TKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEP TPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTT TPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTT Nucleic acids having the sequences of clones isolated from libraries different human tissues, useful in recombinant DNA methodologies. Gaps YWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVYFFK 1170 . 0 Length 551; Human; gene therapy; vaccine; disease treatment; detection. YWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTA-YKNWPESVYFFK Indels Human testes-derived DKFZphtes3_4019 homologue #2. 6 Score 2929; DB 4; Pred. No. 1.1e-66; Example III; Page 892-893; 1095pp; English. Mismatches (GEHU-) GERMAN HUMAN GENOME PROJECT. Ā 41.5%; Scc. 100.0%; Pre 551 99US-0149499P. 99US-0156503P. 18-AUG-2000; 2000WO-IB001496. standard; protein; Conservative (first WPI; 2001-327840/34. Similarity Sequence 551 AA; WO200112659-A2. 18-AUG-1999; 28-SEP-1999; 14-APR-2003 22-FEB-2001 551; Wiemann S; 1123 1003 736 1063 964 856 Н Query Match Best Local 8 504 564 61 Matches g  $\delta$ g à 셤 8 g ò g

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                                                                                                                                                                                             TTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKA
                                                                                                                                                                                                                              TIPKPQKPIKAPKKPKTYKPKTMPRVRKPKTTTPTPRKMTSTMPELNPTSRIAEAMLQTT
                                                             TPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAP
                                                                                                  TTQVTSTTTQDTTPFKITTLXFTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids having the sequences of clones isolated from libraries different human tissues, useful in recombinant DNA methodologies.
 LKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKBPAPT
            TPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAP
                                                                                    TTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEP
                                                                                                                              GVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy; vaccine; disease treatment; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                 homologue #1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human testes-derived DKFZphtes3_4019
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                                                                                                                                                                                                                                                                                                                                                                                  standard;
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activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention
                                                                                                                                                                                                                                     514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTPFKITTLKTTTLAPKVTTTTKKTITTTBIMNKPBETAKPKDRATNSKATTPKPQKPTKA
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                                                                                                                                            Gaps
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0
                                                                                                            Length 546;
                                                                                                                                            Indels
                                                                                                            Score 2920; DB 4;
Pred. No. 1.8e-66;
0; Mismatches 0;
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100.0%; Pr
-+ive 0;
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                                                                                                                 Query Match 41.3
Best Local Similarity 100.
Matches 546; Conservative
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2001WO-US050379
                             2000US-0258920P
                                                 Kuettner KE,
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Matches 538; Conservative
                                    (GLAX ) GLAXO GROUP LID
                                                            WPI; 2002-636585/68.
                                                                 N-PSDB; AAL49079
                                                                                                                                              Sequence 538 AA;
    WO200262847-A2
                    31-DEC-2001;
                            29-DEC-2000;
                                                 Hutchins JT,
            15-AUG-2002
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1012 HMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAF 1072 RGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDIKD 1132 1133 AGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRR 1192 PALNYPVYGEMTQVRRRRFERALGPSQTHTIRIQYSPARLAYQDKGVLANEVKVSILWRG 1252 The present invention provides the protein and coding sequences of human lubrication of joints, and the sequences can be used in the degenerative joint conditions or to delay symptoms of a degenerative point conditions or to delay symptoms of a degenerative positic arthritis, reactive arthritis, rheumatcoid arthritis, gout, spondylarthritis, juvenile arthritis, synovitis, tendonitis, tendonitis, systemic lupus erythematosus, CACP, osteoporosis or trauma. The present sequence is the protein encoded by the human 3' cartilage SZP cDNA 832 892 119 952 179 239 299 419 RGHYFWMLSPESPPSPARRITEVWGIPSPIDIVFTRCNCEGKTFFFKDSQYWRFTNDIKD 359 9 New purified superficial zone protein (SZP) polypeptides, useful for treating degenerative joint conditions, e.g. osteoarthritis, rheumatoid arthritis, goody, spondylarthritis, synovitis, tendonitis, lupus, or osteoporosis. PTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLR TTPETTTAAPKVITKETATTTEKTTESKITATTIQVTSTTTQDTTPFKITTLKTTTLAPKV TTPETTTAAPKWIKETATTIEKITESKITATTIQVISTITQDITPEKITTK-TILAPKV TTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRK PKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKI VEVNPKSEDAGGAEGETP Gaps .; ; DB 5; Length 538; ŗ, Su 0; Indels Schmid TM, Schumacher BL, (RUSH-) RUSH PRESBYTERIAN ST LUKE MEDICAL CENT. 40.4%; Score 2850.9; DB 99.8%; Pred. No. 1e-64; 0; Mismatches Claim 59; Page 86-87; 89pp; English.

1253 LPNVVTSAISLPNIRKPDGYDYYAFSKDQYYNLDVPSRTARAITTRSGQTLSKVWYNCP 1311 This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention ö 173 180 233 293 353 09 οĘ 114 RIKKKPIPKPPVVDEAGSGLDNGDFKVTIPDISTIQHNKVSTSPKITTAKPINPRPSLPP 174 NSDTSKETSLIVNKETTVETKETTTTNKQTSTDGKEKITSAKETQSIEKTSAKDLAPTSK 1 RTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPP Nucleic acids having the sequences of clones isolated from libraries different human tissues, useful in recombinant DNA methodologies. VLAKPTPKABTTTKGPALTTPKEPTPTTPKEPASTTPKEPTTIKSAPTTPKEPATTT VLAKPTPKABITITKGPALITPKEPTPTTPKEPASTIPKEPTTITKSAPITPKEPAPITT KSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPT KSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPT Gaps . 0 Length 513; Human; gene therapy; vaccine; disease treatment; detection. Indels Human testes-derived DKFZphtes3_4019 homologue #3. 39.0%; Score 2757; DB 4; 100.0%; Pred. No. 2.3e-62; ive 0; Mismatches 0; Example III; Page 893; 1095pp; English. (GEHU-) GERMAN HUMAN GENOME PROJECT. Š ABU53254 standard; protein; 513 99US-0149499P 18-AUG-2000; 2000WO-IB001496 (first entry) Matches 513; Conservative WPI; 2001-327840/34. Similarity Sequence 513 AA; WO200112659-A2. 14-APR-2003 Homo sapiens 18-AUG-1999; 28-SEP-1999; 22-FEB-2001 S ABU53254; 234 121 Query Match 61 294 181 Wiemann Local Dp ð 셤 à ò П ò d δ 셤

354 TPKEPAPTTPKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEP 413

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Search completed: October 13, 2004, 11:37:31 Job time : 114.696 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

October 13, 2004, 11:23:49; Search time 22.7891 Seconds (without alignments) 3815.116 Million cell updates/sec Run on:

SEQ1-H 7064 1 MAWKTLPIYLLLLLSVFVIQ......ARALTTRSGQTLSKVWYNCP 1311 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.1 Scoring table:

478139 seqs, 66318000 residues Searched:

478139 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

4.0.0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	US-07-757-022B-42	US-07-757-022B-48	07-757-022B-4	US-07-757-022B-2	US-07-757-022B-62	-970A	US-10-164-595-78	-07-757	US-07-757-022B-44	US-07-757-022B-142	US-07-757-022B-46	US-07-757-022B-60	US-07-757-022B-52	US-10-164-595-58	US-07-757-022B-104	US-07-757-022B-74	US-07-757-022B-84	US-07-757-022B-58	US-07-757-022B-14	US-07-757-022B-54	US-07-757-022B-66	US-07-757-022B-68	US-07-757-022B-64	- (	-07-757-022	-08-714-741-32	-757-022	
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æ	Query	100.0	8.66	8.66	99.7	99.7	99.7	99.5	96.4	96.3	96.1	0.96	96.0	96.0	95.8	79.3	77.9	77.5	75.7	70.9	29.1	25.6	25.4	24.4	19.8	17.3	16.1	15.7	
	Score	7064	7049.7	7049	7044.7	7044.7	7044.7	029.	6811.3	6.6629	6785.6	6784.9	6784.9	6780.6	6.6979	5603.7	5500.7	5472.6	5344.6	5011	2057.8	1806.8	1793.7	1723.1	1398.2	1219.6	1139.7	1108.5	
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102, App 114, App 116, App	136, App 136, App 1, Appli	, Appli 8, Appl	, _ A;	5, Appli 1142, Ap 425, App	Appli Appli	APP11 , APP1 0, APP
		400	1 (1 )			30,
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US-07-757-022B-102 US-07-757-022B-114 US-07-757-022B-116	US-07-757-022B-136 US-09-579-181-1	US-09-3/9-181-2 US-09-919-172-98 US-09-976-594-22	US-09-919-039-21 US-08-928-361B-5	US-09-588-995A-5 US-09-538-092-1142 US-09-854-133-425	US-08-700-651-5 US-08-928-361B-6 US-09-588-995A-6	US-07-757-022B-30 US-07-757-022B-140
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157 157 207	3118	3256	3256	183/ 2142 4019	1721 1721 1721	231
12.5 12.5 12.3	12.3	11.7	11.7	11.5	11.2	10.9
884 884 869	849.6 849.6	824.7	824.7	808.9 808.4	794.6 794.6 794.6	771
28 29 30	31 32 33	34.5	37	0 8 4 0 0 0	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	<b>4</b> 4 5

## ALIGNMENTS

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APPLICANT: Gener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Turner, Katherine
APPLICANT: Hawick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                             Sequence 42, Application US/07757022B Patent No. 6433142 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI 5190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: CSETY, LUADIN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 1311 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                        RY: U.S.A.
02140
RESULT 1
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SPRSPPSPARRITEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIF 1140
                                                                                                                                                                                                 KGFGGLTGQIVAALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVY 1200
                                                               GEMTQVRRRRFERAIGPSQTHTIRIQYSPARLAYQDKGVLHNEVKVSILWRGLPNVVTSA
                                                                                                                                                                                                                                                        SPFSPPSPARRITEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDIKDAGYPKTFF
                                                                                                                                                                       KGFGGLTGQIVAALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVY
                                               FMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWML
                                                                                                                                                                                                                                                                                                1261 ISLPNIRKPDGYDYYAFSKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP 1311
                                                                                                                                                                                                                                                                                                                     RESULT 2
US-07-757-022B-48
Sequence 48, Application US/07757022B
Sequence 48, Application US/07757022B
Sequence No. 643142
GENERAL INFORMATION:
APPLICANT: Gener Thomas G.
APPLICANT: Turner, Katherine
APPLICANT: Hawick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1999
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1999
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
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SOFTWARE: Patences.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
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87 CambridgePark Drive
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TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 48
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 31
REFERENCE/DOCKET NUMBER:
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                                                                        DB 4; Length 1311;
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                                                                       100.0%; Score 7064; DB 4;
100.0%; Pred. No. 4.5e-193;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 1311; Conservative
            TOPOLOGY: linear MOLECULE TYPE: protein
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US-07-757-022B-42
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                                                                                                                  DB 4;
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Pred. No. 1.2e-192;
0; Mismatches 0;
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                                                                                                                              Best Local Similarity 96.8 Matches 1311; Conservative
                                 MOLECULE TYPE: protein
  AMINO ACID
; TYPE: AMING;
; TOPOLOGY: ];
; MOLECULE TYPE:
US-07-757-0228-48
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QGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWG 1097 1200 1217 1320 1157 SQTHTIRIQYSPARLAYQDKGVLHNEVKVSILWRGLPNVVTSALSLPNIRKPDGYDYYAF 1277 **AMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPN ATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPTPKMTSTMPELNPTSRIAE** IPSPIDIVETRCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTA KYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRFBRAIGP 1201 KYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRRFERAIGP APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TTLE OF INTENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 18-910910
CLASSIPICATION NATA:
APPLICATION NUMBER: US 07/643,502
FILING DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
ADDITORATION NUMBER: US 07/457,196 1278 SKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP 1311 901 REGISTRATION NUMBER: 31,822 REFERENCE/DOCKET NUMBER: GI 5190 TELECOMMUNICATION INFORMATION: Sequence 40, Application US/07757022B Patent No. 6433142 GENERAL INFORMATION: ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive APPLICATION NUMBER: US 07/390, FILING DATE: 08-AUG-1989 ATTORNEY/AGENT INFORMATION: CITY: Cambridge STATE: Massachusetts U.S.A. US-07-757-022B-40 COUNTRY: 1021 196 978 1038 1081 1098 1158 1218 Db ò g  $\delta$ g à d ठे Ωp à g ò

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VAALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRR 1210
                                                                                                                                             PTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMD
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         TTEKTTESKITATTTQVTSTTTQDTTPPKITTLKTTTLAPKVTTTKKTITTTEIMNKPEE
                                                                   TAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELN
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APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetian
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-UAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1389
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 08-AUG-1989
FILING DATE: 08-AUG-1989
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FILING DATE: 19910910
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87 CambridgePark Drive
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Patent No. 6433142
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CLASSIFICATION: 530
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US-07-757-022B-2
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CITY: Ca
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                                                                                                                                                Score 7049; DB 4;
Pred. No. 1.3e-192;
0; Mismatches 0;
TELEFAX: (617)876-1170
INFORMATION FOR SEQ ID NO: 40: SEQUENCE CHARACTERISTICS:
LENGTH: 1361 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECUT A.
                                                                                                                                                  Query Match
Best Local Similarity 96.3%;
Matches 1311; Conservative
                                                                                                       MOLECULE TYPE: protein US-07-757-0228-40
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US-07-757-022B-62
i Sequence 62, Application US/07757022B
i Sequence 62, Application US/07757022B
i GENERAL INFORMATION:
APPLICANT: Gener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Turner, Ratherine
APPLICANT: Hewick, Rodney M.
ITLE OF INVENTION: Megakaryocyte Sti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                PSRTARAITTRSGOTLSKVWYNCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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STATE: Massachusetts
COUNTRY: U.S.A.
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MEDIUM TYPE: Floppy
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CLASSIFICATION:
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STREET: 87
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Pred. No. 1.8e-192;
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                                  5190
    NAME: CSCPT, LUADA
REGISTRATION NUMBER: 31,822
REPERRINCE/DOCKET NUMBER: GI 5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 amino acids
TYPE: AMINO ACID
TOPOLOGY: LINEAR
                                                                                                                                                                   99.7%;
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                             Query Match
Best Local Similarity 93.4
Matches 1311; Conservative
                                                                                                                                / MOLECULE TYPE: protein US-07-757-0228-2
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991

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1021 POKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKKMTSTMPELNPTSRIAEAMLOTTTRPN
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ilarity 93.4%; Pred. No. 1.8e-192;
Conservative 0; Mismatches 0;
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; Sequence 1, Application US/09298970A
; GENERAL INFORMATION:
; APPLICAMY: JAY, Gregory D.
; TITLE OF INVENTION: TRIBONECTINS
; FILE REFERENCE: 21486-026
; CURRENT APPLICATION NUMBER: US/09/298,970A
; CURRENT FILING DATE: 2001-06-19
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 1
; SEQ ID NO 1
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Matches 1311; Conserv
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Best Local Similarity 93.4%; Pred. No. 1.8e-192;
Matches 1311; Conservative 0; Mismatches 0;
         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CSETY, LUMBIN
                                                                                                                                                                                                     5190
                                                                                                                                                                   NAME: CSET, Luann
REGISTRATION NUMBER: 31,822
REFRENCE/DOCKET NUMBER: GI 51
TELECOMMUNICATION INPORMATION:
TELEFAX: (617)876-1170
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                1404 amino acids
                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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RESULT 8 US-07-757-022B-50

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FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATE: 407/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/646,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
THING DATE: 19-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 09-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: CREET: LUBBING ATTORNEY/AGENT INFORMATION:
NAME: CREET: LUBBING ATTORNEY/AGENT INFORMATION: Inc 5190 ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive CITY: Cambridge Sequence 50, Application US/0775705;
Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: Gener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryoc;
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS: NAME: CBerr, Luann REGISTRATION NUMBER: 31,822 REFERENCE/DOCKET NUMBER: G1 TELECOMMUNICATION INFORMATION: TELEPHONE: (617)876-1170 Query Match
Best Local Similarity 96.0%;
Matches 1278; Conservative : 1314 amino acids AMINO ACID 61 KRVCTAELSC-----TELEFAX: (617)876-5851 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: MOLECULE TYPE: protein US-07-757-0228-50 STATE: Massachusetts COUNTRY: U.S.A. COMPUTER READABLE FORM: MEDIUM TYPE: Floppy TELEPHONE: TOPOLOGY: 161 19 g à seq1-h.rai

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80 PKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINFRPSLPFNSDTSKE 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41;
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                                                                                   APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.3%; Score 6799.9; DB 4 96.9%; Pred. No. 1.4e-185;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATE: US 07/546,114
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/457,196
                                                                                                                                                                                                                                                  E: Genetics Institute, Inc.
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTOMNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5190
                    Sequence 44, Application US/07757022B
Patent No. 6433142
GENERAL INFORMATION:
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REGISTRATION NUMBER: 31,822
REFRENCE/DOCKET NUMBER: GI 5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-5851
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1270 amino acids
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Best Local Similarity 96.9
Matches 1270; Conservative
                                                                                                                                                                                                                                                                                                                     Massachusetts
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TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-0228-44
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                             ADDRESSEE: Generis
STREET: 87 Cambri
CITY: Cambridge
STATE: Massachuse
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US-07-757-022B-44
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1220 ISLPNIRKPDGYDYYAFSKDQYYNIDVPSRTARAITTRSGQTLSRVWYNCP
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                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT AFPLICATION DATA:
PEPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 08-NUG-1989
ATICHED APPLICATION NUMBER: US 07/457,196
FILING DATE: 08-NUG-1989
ATICHED APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-NUG-1989
ATICHED APPLICATION NUMBER: US 07/390,901
FILING DATE: US 08-NUG-1989
                                                                                                                                                                                                                                                                                                  Inc
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                                                                                                                Sequence 142, Application US/07757022B Patent No. 6433142
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                    3: Genetics Institute,
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 142: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1313 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (617)876-5851
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Best Local Similarity
Matches 1270; Conserv
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US-07-757-022B-142
                                                                                   RESULT 10
US-07-757-022B-142
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                                                                                     KAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTP
                                                                                                                                                                                TTPKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKE
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                                       140 TSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTP
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                                             1278 SKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 29-UN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-0AN-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                              ; Sequence 46, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 31,822
REFRENCE/DOCKET NUMBER: GI 5:
TELECOMMUNICATION INFORMATION:
TELEPAN: (617)876-1170
TELEPAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 29-JUN
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APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS: CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
PRICATION: 530 DB 4; 1311 Score 6784.9; DB 4, Pred. No. 3.9e-185;

QY   1151 VAALSTAKYKUWPESVYFFKRGGSIQQYIYKQEPVCKCPGRRPALNYPVYGEMTQVRRRR	RESULT 12  OS-7-52-022B-60  Sequence 60,439,42  FREEZEA, INPORMATION: APPLICANT: Clark, Stephen C. APPLICANT: Clark, Stephen C. APPLICANT: Hewick, Rachering APPLICANT: Hewick, Rachering APPLICANT: Hewick, Rachering APPLICANT: Hewick, Rachering APPLICANT: Hewick, Rachering APPLICANT: Hewick, Rachering CORRESED Genetics Institute, Inc. STATE: Massachusetts ADDRESSE: Genetics Institute, Inc. STATE: Massachusetts STATE: Massachusetts CORNUTER READABLE FORM: APPLICATION NUMBER: OS OFFASSO OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PS-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING DATE: 29-DOS-199 FILING D	Query M Best Lo Matches
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1040 YLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPAR 1099
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                                      RITEVWGIPSPIDIVFTRCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQI
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-78N-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-40N-1990
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APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
FILOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEB: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge CITY: Massachusetts
                                                                                                                                                                                                                                                                                                  ; Sequence 52, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Gener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte St
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION: TELECOMMUNICATION: (617)876-1170
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
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GY: linear
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US-07-757-022B-52
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                                                                                  DETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFT
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RCNCEGKTFFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVY
                                  QTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFWPEVTPDMDYLPRVPNQGIIINPMLS
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                                                                                                                                                                                                                                                                                                                                                           Sequence 58, Application US/10164595; Sequence 58, Application US/10164595; Patent No. 6657054; GENERAL INFORMATION:
APPLICANT: Oricene Technologies, Inc.
TILLE OF INVENTION: Regulated Angiogenesis Ger.; FILE REFERENCE: 10 103 R1
CURRENT APPLICATION NUMBER: US/10/164,595; CURRENT FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58
                                                                                                                                                                                                                                                                                PSRTARAITTRSGQTLSKVWYNCP 1311
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Best Local Similarity 93.1
Matches 1267; Conservative
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; ORGANISM: Homo sapiens
US-10-164-595-58
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US-10-164-595-58
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                                                      MAWKTLPIYLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF
                                                                                                                    --VKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTST
                                  Gaps
         Length 1363;
                                  134;
                                  Indels
                                                                                                        KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAE-
            DB 4;
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            6780.6; DB 4
No. 5.5e-185;
                                  0; Mismatches
             Score
Pred.
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            Query Match
Best Local Similarity 90.5%;
Matches 1270; Conservative
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APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Ratherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                           COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                       CITY: Cambridge
STATE: Massachus
COUNTRY: U.S.A.
           GENERAL INFORMATION:
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STREET: 87
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Patent No.
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#1.25

E: Genetics Institute, 87 CambridgePark Drive

Massachusetts

106 121 PPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEEHSVSENQESSSSSSSSSSSTIW 180 -----VKDNKKONRIKKKPTPKPPVVDEAGSGLDNGDFKVTTPDIST 147 181 KIKSSKNSAANRELQKKLKVKDNKKNRTKKKPTPKPPVVDBAGSGLDNGDFKVTTPDTST 240 TQHNKVSISPKITTAKPINPRPSLPPNSDISKETSLIVNKETTVETKETTTTNKQTSIDG 207 9 1 MAWKTLPIYLLLLISVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF Gaps 93; 61 KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAE---0; Indels Score 5603.7; DB 4; Pred. No. 1.3e-151; 0; Mismatches 0; NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5951 INFORMATION FOR SEQ ID NO: 104 Query Match 79.3%; Best Local Similarity 91.8%; Matches 1047; Conservative C 1140 amino acids SEQUENCE CHARACTERISTICS: LENGTH: 1140 amino acio TOPOLOGY: linear; MOLECULE TYPE: protein US-07-757-022B-104 AMINO ACID 148 107 107 ö g

RESULT 15 US-07-757-022B-104 ; Sequence 104, Application US/07757022B

QHNKVSTSPKITTAKPINPRP	KEKTTSAKETOSIEKTSAKDLAPTSKVLAKPPRAETTTKGPALTTPKEPTSTTPKEPAS 267	KTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEFTFTTFKEFAS 36	TTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTTKEPAPTTTKEP 327 	TITIKSAPITPKEPAPITPKEPAPITPKEPAPITPK 3	TPK	APT 44	PAPT 54	TTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKP 507		APTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTT 567	PTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTT 66		BEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEP 7	PITPKKDAPKELAPITIKEPISITSOKBAPITPKGIAPITPKEPAPITPKG 68	KEPAPTTPKG 78	SDKPAPITPKETAPITPKEPAPITPK 74	TAPTTLKEPAPTTPKKPAPKBLAPTTTKGPTSTTSDKPAPTTPKBTAPTTPKBPAPTTPK 840	MSPKEPGVPT 80	KPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPT 900		TKTPAATKPEMTTTAKOKTTERDLRITPBTTTAAPKWIKETATTTEKTTESKITATTTQV 960	927	STTQDTTPFKITTLKTTTLAPKVTTTKKTITTTBINNKPEETAKPKDRATNSKATTPK 10	OKPIKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIABAMLQTTTRPN	OTTTREN 1	PDMSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDXLPRVPNQGIIINPMLS	
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Search completed: October 13, 2004, 11:59:29 Job time: 29.7891 secs

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GenCore version 5.1.6
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1356558 seqs, 322682953 residues

Total number of hits satisfying chosen parameters: length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

1356558

Published Applications AA:*

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| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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| cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:* Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 30, Appli Sequence 1, Appli Sequence 2, Appli Sequence 62, Appl Sequence 44, Appl Sequence 142, Appl Sequence 142, Appl Sequence 60, Appl Sequence 52, Appl Sequence 52, Appl Sequence 52, Appl Sequence 40, A Sequence 30, A Sequence 1, A Sequence 2, A Sequence 42, Sequence 48, Description 3 US-10-124-557-42 3 US-10-124-557-48 3 US-0-802-207-30 US-09-802-207-30 US-09-897-188-1 3 US-10-124-557-2 3 US-10-124-557-62 US-10-124-557-44 US-10-124-557-46 US-10-124-557-60 US-10-124-557-60 US-10-124-557-60 US-10-124-557-60 US-10-124-557-60 Query Match Length DB 1311 1354 1361 1404 1404 1404 1404 1314 1313 1320 1320 1363 100.0 99.8 99.8 7.99.7 7.99.7 Score 7044.7 7044.7 7044.7 6811.3 6799.9 6785.6 6784.9 6784.9 7049.7 7049 7044.7 8 110 111 14 14 Result

Section 2	# *	Seguence 84, Appl	0 -	יו נו	7	n L	י מ	ا م		ָ ט	) v	Sequence 100	ocducation To	oednence Tr	Sequence 1.	seduence 4	/ eadnesice	Sequence 70	z ednence z	sednence 4	Sequence 108, App	5784,	Sequence 5013, Ap	Sequence 5, Appli		Sequence 102, App	Segmence 114 App	Agrical a social pass	5 ,		ń	Sequence 2318, Ap
.3 US-10-124-557-74	-10-124-557	3 US-10-124-557-	-10-124-5		4 US-10-038-694	US-10-124-557-	IIS-10-124-557-	TIS-10-124-EF7-C	οv	US-09-R02-20	US-09-922-21	US-09-833-263-1068	3 US-10-025-380-1068	6 US-10-734-564-121	16 US-10-468-910-4	3 IIS-10-124-557-72	3 US-10-124-557-70	4 US-10-038-694-2	4 IIS-10-295-023-429	9 IIS-09-801-369-109	119-10-269-403-F	14 TE-10-369-493-5764			US-09-864-761-356	US-10-124	$\Omega S - TC$	US-10-243	IIS-10-142-515-1	712	0 410 400 11 011 011 011 011 011 011 011	7
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## ALIGNMENTS

Sequence 42, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS: COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READBAILE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: Unknown>
PRIOR APPLICATION: Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-DEC-1999
APPLICATION NUMBER: US 07/857,196
FILING DATE: 09-DEC-1999
APPLICATION NUMBER: US 07/857,196
FILING DATE: 09-DEC-1999
APPLICATION NUMBER: US 07/857,196
FILING DATE: 09-DEC-1999
APPLICATION NUMBER: US 07/857,196
FILING DATE: 08-AUG-1989 ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive CITY: Cambridge STATE: Massachusetts US-10-124-557-42

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SPFSPPSPARRITEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIF
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:

PRIOR APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: CURNOWN>
PRIOR APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UWN-1990
APPLICATION NUMBER: US 07/545,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
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Hewick, Rodney M.
Geener, Thomas G.
TITLE OF INVENTION: MEGAKARYOCYTE NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-124-557-48
; Sequence 48, Application US/10124557
; Publication No. US20220137894A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Turner, Katherine Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Cambridge
STATE: Massachusetts
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                                                                                                                                                                                                                                  ; Score 7064; DB 13; Length 1311;
; Pred. No. 3e-163;
0; Mismatches 0; Indels 0;
                                                        5190
                                                                                                                                                              TOTOLOGY Innear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 42:
                           NAME: CSETT, LUANN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 51;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEPAX: (617)876-1170
TELEPAX: (617)876-1170
TELEPAX: (617)876-1170
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TELEPAX: (617)876-1170
TELEPAX: (617)876-1170
TELEPAX: (617)876-1170
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 1311 amino acids
                                                                                                                                                                                                                                     Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1311; Conservative 0
                                                                                                                                                          TYPE: amino acid
                  ATTORNEY/AGENT
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AMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPN 1037
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                                            NSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTE
                                                                 841 NSPKEPGVPTTKTPAATKPEMTTTAKDKTTBRDLRTTPETTTAAPKMTKSTATTTEKTTE
                                                                                              SKITATTIQVISTTIQDTTPFKITTLKTTTLAPKVTTTKKTITTTBIMNKPEETAKPKDR
                                                                                                               KYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRRFERAIGP
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-0AN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSER: Genetics Institute, In
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte St
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 40, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
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                                                                                                                                                                                                       Score 7049.7; DB 1:
Pred. No. 6.9e-163;
0; Mismatches 0;
                                       5190
                                                                                                                                                                     48:
         NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                       INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 1354 amino acids
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                       99.8%;
                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                  Best Local Similarity 96.8
Matches 1311; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETAT
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                                                                                                                                                                                                       TAKPKDRATNSKATTPKPOKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELN
                                                                                                                                                                                                                                                          PTSRIABAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMD
                                                                                                                                                                                                                                                                                                                                                                  RITEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLIGQI
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                                                           Length 1404;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
99.7%; Score 7044.7; DB 9;
Best Local Similarity 93.4%; Pred. No. 9.6e-163;
Matches 1311; Conservative 0; Mismatches 0;
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US-09-802-207-30

| Sequence 30, Application US/09802207
| Publication No. US20020086824A1
| GENERAL INFORMATION:
| APPLICANT: Warman, Matthew
| APPLICANT: Carpten, John
| APPLICANT: Trent, Jeffrey
| APPLICANT: Marcelino, Jose
| TITLE OF INVENTION: NOVel Methods and Reagents for FILE REFERENCE: Case-06212
| CURRENT APPLICATION NOWBER: US/09/802,207
| CURRENT APPLICATION NUMBER: 09/619,175
| PRIOR PAPLICATION NUMBER: 09/619,175
| PRIOR PILING DATE: 2000-07-19
| PRIOR APPLICATION NUMBER: 66/145,328
| PRIOR APPLICATION NUMBER: 66/145,328
| RECOR FILING DATE: 1999-07-23
| NUMBER OF SEQ ID NOS: 30
| SOFTWARE: PatentIn version 3.0
| SEQ ID NO 30
| LENGTH: 1404
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ORGANISM: Homo sapiens
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99.8%; Score 7049; DB 13;
Best Local Similarity 96.3%; Fred. No. 7.2e-163;
Matches 1311; Conservative 0; Mismatches 0;
           APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                             NAME: CBETT, LUADIN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-5851
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                             40:
                                                                                                                                                                                          TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-124-557-40
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Pred. No. 9.6e-163;
0; Mismatches 0; Indels 93; 0
                                                                                                                                                       DF INVENTION: Megakaryocyte Stimulating Factors OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-DAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DC-1989
APTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              Inc
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APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIPICATION: <Unknown>
                                                                                                                                                                                                            ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive
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SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-124-557-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
       Sequence 2, Application US/10124557; Publication No. US20020137894A1
GENERAL INFORMATION:
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
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                                                                                                                                                                                                                                              CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
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SEQUENCE CHARACTERISTICS:
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Best Local Similarity 93.4%;
Matches 1311; Conservative (
                                                                                                                                                           TITLE OF INVENTION: Meg
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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US-10-124-557-2
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                                                                                                                                                                                             Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAE
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APPLICATION DATA:

APPLICATION NUMBER: US/10/124,557

FILING DATE: 16-Apr-2002

CLASSIFICATION CURROWN-

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502

FILING DATE: 29-UN-1991

APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-UN-1990

APPLICATION NUMBER: US 07/57,196

FILING DATE: 29-DEC-1999

APPLICATION NUMBER: US 07/457,196

FILING DATE: 29-DEC-1999

APPLICATION NUMBER: US 07/590,901

FILING DATE: 29-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                      ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUWTRY: U.S.A.
ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62:
                                                  PSRTARAITTRSGQTLSKVWYNCP 1311
                                                              NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                  Sequence 62, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
                                                                                                                                                                     APPLICANT: Turner, Katherine Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617)876-5851
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LENGTH: 1404 amino a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 93.4 Matches 1311; Conservative
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                                                   FPKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRRFERAIGPSQTHTIRIQY
                                                                                                      SPARLAYODKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYYAFSKDQYYNIDV
               Length 1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5190
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US-10-124-557-50

Sequence 50, Application US/10124557

Sequence 50, Application US/10124557

Publication No. US20020137894A1

GENERAL INFORMATION:

APPLICANT: Turner, Katherine

Clark, Stephen C.

Jacobs, Kenneth

Hewick, Rodney M.

Gesner, Thomas G.

TITLE OF INFORTION: Megakaryocyte Sti

NUMBER OF SEQUENCES: 143

CORRESPONDENCE ADDRESS:
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-124-557-50
                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genetics Institute,
STREET: 87 cambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                        1404
                                                                                                                                                              PSRTARAITTRSGQTLSKVWYNCP 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                               1381 PSRTARAITTRSGQTLSKVWYNCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (617)876-1170
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MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-124-557-142
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TOPOLOGY: linear
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                                                   1 MAWKILPIYLLILLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF
                                 Gaps
             DB 13; Length 1270;
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             Score 6799.9; DB 1. Pred. No. 7.2e-157;
                                 0; Mismatches
                                                                    MAWKTLPIYLLLLSVFVIQQVSSQ-
              96.3%;
96.9%;
                 96.3
Dest Local Similarity 96.9
Matches 1270; Conservative
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FMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHXFWML
                              SPESPPSPARRITEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIF
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                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 16-Apr-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-0AN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142:
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REGISTRATION NUMBER: 31,822
REGISTRATION OF THE TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 142, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
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COUNTRY: U.S.A.
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Page

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AMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPN 1037
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                                                                  1098 IPSPIDTVFTRCNCEGKTPFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTA
                                                                                                                     1100 IPSPIDIVFTRCNCBGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTA
                                                                                                                                                                             1160 KYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRRFERAIGP
                                                                                                                                                       KYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRFFERAIGP
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC comparible
COMPUTER: TBM FC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: CURROWN>
                                                                                                                                                                                                                                                                                                                                                  Sequence 46, Application US/10124557
Fublication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Facil
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                            SKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP 1313
                                                                                                                                                                                                                                                             SKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP 1311
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-7M-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1889
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-NUG-1889
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 amino acids
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STATE: Massachusetts
COUNTRY: U.S.A.
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        DB 13; Length 1313;
                                  84;
                               Indels
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    Score 6785.6; DB 1.
Pred. No. 1.7e-156;
0; Mismatches 0;
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  96.1%;
93.8%;
                         Matches 1270; Conservative
               Similarity
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Best Local (
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                                                                                                         YLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPAR
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                      TAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELN
                                                    PTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMD
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ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                               GYDYYAFSKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Megakaryocyte Stimulating INUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESSE:
ADDRESSE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR DATE: 16-Apr-2002
CLASSIFICATION INDMER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION ADMER: US 07/643,502
PILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT TRORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5190
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 60, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
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STATE: Massachusetts
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                                                                                                                                                                                     61 KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCA-------
                                                                             Length 1320;
                                                                                                        91;
                                                                                                         Indels
                                                                              13;
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                                                                           Score 6784.9; DB 1:
Pred. No. 1.8e-156;
0; Mismatches 0;
                 MOLECULE TYPE: protein SEQ ID NO: 46: US-10-124-557-46
                                                                                                                                                       1 MAWKTLPIYLLLLLSVFVIQQVSSQ-
                                                                               96.0%;
93.3%;
              TOPOLOGY: linear
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                                                                                               Local Similarity
                                                                                                            Matches 1270;
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                                 860 TTEKTTESKITATITQVTSTITQOTTPFKITTLKTTTLAPKVTTTKKTITTEIMVKPEE
                                                                                                TAKPKDRATUSKATIPKPQKPIKAPKKPTSIKKPKIMPRVRKPKTTPIPRKMTSIMPELN
                                                                                                                              PTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMD
                                                                                                                                                 VAALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRR
                                                                     TAKPKDRATNSKATTPKRPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPBLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 52, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            1311
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
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REGISTRATION NUMBER: 31,822
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US-10-124-557-52
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                                                                                                                                   96.0%; Score 6784.9; DB 13; Length 1320;
93.3%; Pred. No. 1.8e-156;
.ive 0; Mismatches 0; Indels 91;
                                                                                            9
            SEQUENCE CHARACTERISTICS:
| FARMORTH: 1320 amino acids |
| TYPE: amino acid |
| TYPE: amino acid |
| TOPOLOGY: linear |
| MOLECULE TYPE: protein |
| SEQUENCE DESCRIPTION: SEQ ID NO: US-10-124-557-60
                                                                                                                                                                                                                       1 MAWKTLPIYLLLLSVFVIQQVSSQ-
INFORMATION FOR SEQ ID NO: 60:
                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 1270; Conserv
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                                                            RCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVY
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KPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPT
                                                TKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKLTATTTQV
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COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/10/124,557
FILING DATE: 16-APY-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18.JAN-1991
APPLICATION NUMBER: US 07/546,114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte St
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
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STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
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Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
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COMPUTER READABLE FORM:
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US-10-124-557-104
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                                                                                                                                                                                           Gaps
                                                                                                                                                                  Query Match

96.0%; Score 6780.6; DB 13; Length 1363;
Best Local Similarity 90.5%; Pred. No. 2.3e-156;
Matches 1270; Conservative 0; Mismatches 0; Indels 134;
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                                                                                                                                                                                                                                   1 MAWKTLPIYLLLLSVFVIQQVSSO--
                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1363 amino acids
          REFERENCE/DOCKET NUMBER:
                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
US-10-124-557-52
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QTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLS 1047
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                                           APTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKG
                APTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKBPAPTTPKG
                                                                              TAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPK
                                                                                                          TAPTILKEPAPTIPKKPAPKELAPTITKGPISTTSDKPAPTIPKETAPTIPKEPAPTIPK
                                                                                                                                         KPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPT
                                                                                                                                                               TSTTTQDTTPPKITTLKTTTLAPKVTTTTKKTLTTTBIMNKPBETAKPKDKATTPK
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MEDIUM TYPER FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kanneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-7M-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DC-1989
APPLICATION NUMBER: US 07/457,196
FILING DATE: 09-AUG-1989
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5190
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-1876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 74, Application US/10124557; Publication No. US20020137894A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                           93; Gaps
                                                                                                                                                                                                                                                                                                                                     79.3%; Score 5603.7; DB 13; Length 1140; larity 91.8%; Pred. No. 6.4e-128; Conservative 0; Mismatches 0; Indels 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRVCTABLSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAE---
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1889
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1889
ATTORNEY/AGENT INFORMATION:
                                                                                                                                   5190
                                                                                                                                                                                                                           LENGTH: 1140 amino acids

TYPE: amino acid

TOPOLOGY: Linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 104:
                                                                                        NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 51.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
                                                                                                                                                                         TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 1047; Conserv
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                                                                                                 1 MAWKTLPIYLLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF
                                                                    DB 13; Length 1038;
                                                                                    Indels
                                                                   Score 5500.7; DB 13
Pred. No. 1.8e-125;
0; Mismatches 0;
                                                                                                            ; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1038 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 74:
                                              74:
                                                                     Query Match 77.9%;
Best Local Similarity 79.2%;
Matches 1038; Conservative
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completed: October 13, 2004, 11:53:32 ne : 142.379 secs Search cor Job time

## GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

October 13, 2004, 11:23:49 ; Search time 144.144 Seconds (without alignments) 5233.063 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

SEQ1-H 7064 1 MAWKTLPIYLLLLLSVFVIQ......ARAITTRSGQTLSKVWYNCP 1311

BLOSUM62 Gapop 10.0 , Gapext 0.1 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	neines omod \$29290	o Hou	Since Chicago	α			٦.			O7ktf6 drosonhila		O7mmd5 anombeles &	Ofssek chlamydomon	Aas 07044 chlamidom	Offit hos taining	Aas8397 hos taurus	O06852 clostridium		7	Oghcat homo sanion	O8wwq4 homo sanien	drosc	۰,		_		~		ם נו	OBwa42 homo sanion	drosc
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Q10465 homo sapien Q7qkk7 anopheles g Q8h6d5 phytophthor Aap74661 phytophth P70670 mus musculu Q96449 phytophthor Q20007 caenorhabdi Q757n5 ashbya gos Aas52662 ashbya gos Q9823 drosophila Q8isf5 caenorhabdi Q911e9 arabidopsis	V81s16 caenorhabdi Q8isf7 caenorhabdi
Q10465 Q7QKK7 Q7QKK7 Q8HQS AAP74661 P70674 Q706749 Q75705 Q75705 Q952062 Q9W2Z3 Q8U2Z5 Q9W2Z3	Q8ISF7
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## ALIGNMENTS

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pfam; PF010043; Somatomedin B; 2.
PRINTS; PR00022; SOMATOMEDINB.
SMART; SM00120; HX; 2.
SMART; SM00201; SO; 2.
SMART; SM00201; SO; 2.
SMART; SM00201; SO; 2.
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SMART; SM00201; SO; 2.
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SMART; SM00201; SO; 2.
SMART)MIN B; 2.
SEQUENCE 1404 AA; 151076 MW; 782A11746B3FDEE5 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
BG174L6.2 (MSF: megakaryocyte stimulating factor ).
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Pred. No. 2.9e-139;
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Submitted (JUL-2000) to the EMBL/(
EMBL; AL133553; CAC36090.1; -.
HSSP, Pol0049; 10C0.
InterPro; IPR001585; Hemopexin.
InterPro; IPR001212; Somatomedin_
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Best Local Similarity
Matches 1308; Conserv
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            Score 7044.7; DB 2
Pred. No. 1.4e-139;
0; Mismatches 0;
                Query Match
Best Local Similarity 93.4%;
Matches 1311; Conservative
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Senoh A., Mizuguchi H., Inagaki H., Sugiyama T.,
Seno H., Wakamatsu A., Ishii S., Yamamoto J.,
Y., Satico K., Nishikawa T., Kimura K.,
o K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
awa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
mi B., Suzuki Y., Sugano S., Nagahari K.,
Isogai T.;
Loogai T.;
Loo the EMBL/GenBank/DDBJ databases.
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imates, Catarrhini, Hominidae, Homo.
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512 MW; B883773C5BC21A23 CRC64;
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1. 27, Last sequence update)
1. 27, Last annotation update)
1.116561.
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Db 910 PSRTARAITTRSGQTLSKVWYNCP 933	5 4	BAD18580; 12-MAY-2004 (TrEMBLrel. 27, Created) 12-MAY-2004 (TrEMBLrel. 27, Last sequence update) 12-MAY-2004 (TrEMBLrel. 27, Last annotation update)	CDNA FLJ16561 fis, clone SYNOV400 sapiens proteoglycan 4, (megakar) superficial zone protein, camptoo superficial cone protein, camptoo superficial conference (ppg)	DE pericarditis Synatomes (Prost).  OS Homo sapiens (Human).  OC Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Eukaryota, Eutheria; Primates; Catarrhini; Hominidae; Homo.  OX NCBI_TaxID=9606;	RN [1] RP SEQUENCE FROM N.A. RC TISSUE=Synovial membrane tissue; RA Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T.,	RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., RA Yamashita H., Matsuo K., Makamura Y., Sekine M., Kikuchi H., Kanda K.,		DR EMBL, AK131434; BAD18580.1; SQ SEQUENCE 933 AA; 102512 MW; B883773C5BC21A23 CRC64;	Query Match 61.9%; Score 4370.6; DB 2; Length 933; Best Local Similarity 59.8%; Pred. No. 1e-83; Matches 839; Conservative 0; Mismatches 1; Indels 564; Gaps 3;		CDAQCKKYDKCCPDYESFCAB1	Db 26ELSCKGRCFESFERGRECDCDAQCKKYDKCCPOYESFCAEVHNPTSPPSSKKAP 79 Qy 107 106		Qy 107VKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTST 147	Db 200 TQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDG 259  Qy 208 KEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPAPTTTPKEPAS 267		Qy 268 TIPKEPIPTIIKSAPITIPKBPAPITIKSAPITIPKEPAPITITKEPAPITIPKEPAPITITKEP 327	328 APITIKSAPITPKBPAPITPKKPAPITPKEPAPITPKEPTTPKEPTTTPKBPAPITKBPAPITPK	Db 371 370 Oy 388 EPAPTAPKKPAPTTPKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPT 447	Db 371 370
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OX NCBI_TaxID=10090; RN [1] RP SEQUENCE FROM N.A. RX MEDLINE=20573856; PubMed=11124536; RA IRegawa S., Sano M., Koshizuka Y., Nakamura Y.; RT "Isolation, characterization and mapping of the mouse and human PRG4 RT (proteoglycan 4) genes."; RL Cytogenet. Cell Genet. 90:291-297(2000). DR RSP: PO44004; 10C0. DR MGD; MGI:1891344; Prg4. DR InterPro; IPR000585; Hemopexin. DR InterPro; IPR00121212; Somatomedin_B. DR Pfam; PF01033; Somatomedin_B; 2.	DR PRINTS; PR00022; SOWATOMEDINB.	03	
371 508 371 568 371 568 371	TAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKE  KPAPTTPETPPPTTSEVSTPTTTKEPTTHKSPDESTPELSAEPTPKALENSP- PAPTTPETPPPTTSEVSTPTTTKEPTTHKSPDESTPELSAEPTPKALENSP- FALPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKI- FKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKI- FKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKI- TSTTTQDTTPFKITTLAPKWTTTKKTITTTEIMNKPEETAKPKDRATN- FILL	108 RCNCEGKTPFFKDSQYWRFTNDIKDAGYPKDFIFKGFCGLTGQIVAALSTAKYKN 1108 RCNCEGKTPFFKDSQYWRFTNDIKDAGYPKPIFKGFCGLTGQIVAALSTAKYKN 730 RCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFCGLTGQIVAALSTAKYKN 1168 FFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVGEMTQVRRRFFERAIGPSQTF 790 FFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVGEMTQVRRRFFERAIGPSQTF 790 FFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVGETTQVRRRFFERAIGPSQTF 1228 SPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYYAFSKDG 850 SPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYYAFSKDG 850 SPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYYAFSKDG 1288 PSKTARAITTRSGQTLSKVWYNCP 933 1089 Q9JM99 Q9JM99 PRELIMINARY; PRT; 1054 AA. Q9JM99 Q9JM99 Q9JM99 PRELIMINARY; PRT; 1054 AA. Q9JM99 O1-OCT-2000 (TrEMBLrel. 15, Last sequence update) Name=Prg4; Mus musculus. Name=Prg4; Mus musculus (Mouse). Bukaryota; Metazoa; Chordata; Craniata; Wertebrata; Buteleostom Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	

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MEDLINE=99120896; PubMed=9920774;
MEDLINE=99120896; PubMed=9920774;
Plannery C.R., Hughes C.E., Schumacher B.L., Tudor D., Aydelotte M.B.,
Kuettner K.E., Caterson B.;
"Articular cartilage superficial zone protein (SZP) is homologous to
megakaryocyte stimulating factor precursor and Is a multifunctional
proteoglycan with potential growth-promoting, cytoprotective, and
lubricating properties in cartilage metabolism.",
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.

VCBI_TaxID=9913;
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(TremBlrel. 08, Last sequence update)
(TremBlrel. 26, Last annotation update)
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SRIABAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYL 1032
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MEDIJNE=94132002; PubMed=8300571;
Gum J.R. Jr., Hicks J.W., Toribara N.W., Siddiki B., Kim Y.S.;
Gum J.R. Jr., Hicks J.W., Toribara N.W., Siddiki B., Kim Y.S.;
"Molecular cloning of human intestinal mucin (MUC2) cDNA.
Identification of the amino terminus and overall sequence similarity
to prepro-von Willebrand factor.";
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Bukaryota, Metazoa; Onordata, Craniata; Vertebrata, Euteleostomi;

Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo.

NCBL_TaxID=9606;
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                                                                                                                                                                                  "Immunodetection and partial cDNA sequence of the proteoglycan, superficial zone protein, synthesized by cells lining synovial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.3%; Score 1714.7; DB 2; Length 80.2%; Pred. No. 1.3e-28; rive 24; Mismatches 52; Indels
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                                                                                                                                Schumacher B.L., Hughes C.E., Kuettner K.E., Caterson
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Commun. 254:535-541(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
                                                                              TISSUE=Articular cartilage;
MEDLINE=99171663; PubMed=10073655;
                                                                                                                                                                                                                                                     joints.";
J. Orthop. Res. 17:110-120(1999)
EMBL; AF056218; AAD13404.1; -.
InterPro; IPR000585; Hemopexin.
Pfam; PP00045; Hemopexin; 2.
SMART; SM00120; HX; 2.
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les 320; Conservative
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502 LOVQLAPVMQLFVTLDQASQ--GQVQGLCGNFNGLEGDDFKTASGLVEATGAGFANTWKA 559
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82; Mismatches 507; Indels 1248; Gaps
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1504 1504 M -> T (in Ref. 3).
4192 4192 G -> S (in Ref. 2).
5179 AA; 540295 MW; 85CD7571FB9A5663 CRC64;
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                                                                                                                                                                                                 REQUENCE OF 1343-1895 AND 4176-4195 FROM N.A.

REQUIRE 91358717; PubMed=1885763;

RA Toribara N.W., Gum J.R. Jr., Culhane P.J., Lagace R.E., Hicks J.W.,

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RA Toribara N.W., Gum J.R. Jr., Culhane P.J., Lagace R.E., Hicks J.W.,

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RA SECRETALITY: Colon, Small intestine, colonic tumors,

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RA SIMILARITY: Contains 1 TIL (Trypsin inhibitory-like) domain.

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                                                                     MEDLINE=93016, pubMed=1400449, MEDLINE=93016, i. Lagace R.E., Kim Y.S., Kir Y.S., Kim Y.S., Toribara N.W., Rothe E.-M., Lagace R.E., Kim Y.S., "The human WUC2 intestinal mucin has cysteine-rich subdomains located both upstream and downstream of its central repetitive region."; J. Blol. Chem. 267:21375-21383 (1992).
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Mucin 2.
APPROXIMATE REPEATS.
                                     SEQUENCE OF 626-1895 AND 4196-5179 FROM N.A. TISSUE=Colon;
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PROSITE: PSO1225; CTCK_2; 1.
PROSITE: PSO0022; EGF 1; UNKNOWN_1.
PROSITE: PSO1208; VWFC_1; 2.
PROSITE; PS50184; VWFC_2; 2.
GLYCOPTOTEIN: Repeat; Signal siGNAL
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INTERPRO 1 PR002919; Cysrich TIL.
INTERPRO 1 PR006299; Cysrich TIL.
INTERPRO 1 PR006209; Cys knot.
INTERPRO 1 PR006209; EGF_like.
INTERPRO 1 PR001009; EGF_like.
INTERPRO 1 PR00109; WWF_C.
INTERPRO 1 PR0010846; VWF_D.
PFam; PF00097; Cys_knot; 1.
PFam; PF00093; VWC; 1.
PFam; PF00094; VWD; 4.
SWART; SW00214; VWC; 2.
SWART; SW00214; VWC; 2.
Biol. Chem. 269:2440-2446(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L21998; AAB95295.1; --
EMBL; M74027; AAA59875.1; --
EMBL; M94131; AAA59163.1; --
EMBL; M94132; AAA59164.1; --
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Genew; HGNC:7512; MUC2.
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2730 TTTTTVTPTPTPTGT 2744

1090 RRITEVWGIPSPIDT

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RA SECURINCE FROM N.A.

RA AGENGRACE FROM N.A.

RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanarides P.G., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,

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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfelifer B.D.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Flannoch C.B., Baldwin D.,

RA Ballew R.M., Banos P.V., Bernas B.P., Bhandari D., Bolthakov S.,

RA Berson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolthakov S.,

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RA Berlis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chadra I.,

RA Berlis S., Delcher A., Deng Z., Mays A.D., Dew I., Diez S.M.,

Burtis K.G., Busam D.A., Eugen S., Dankov B.C., Dunn P.,

RA Borkova D., Botcher A., Domnes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Glodk A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodk A., Gorrell J.H., Gu Z., Kemison J.A., Retchman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvy D., Herman T.J., Hernandez J.R., Houck J.,

RA Kimmel B.E. Kodira C.D., Karft C., Karvitz S., Kulp D., Lai Z.,

Liu X., Mattei B., McInton T.C., Murny D.M., Necherson D. M.,

RA Mount S.M., Moy M. Murphy B., Murphy L., Murny D.M., Neches M.G.,

RA Bazzolo M., Murphy B., Murphy L., Murny D.M., Neches M.S.,

RA Briazolo M., Pittama J., Mozley K.C., Wu D., Strong R., Sucheler F., Shen H.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Wang X.,

Wallsams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA Beng S.M., Woodager, Wolley R., Willessenbach J.,

Wallbar S.M., Wyers E.W., Rubin G.M., Vener B., Zhu X., Sath H.O.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhon B.,

Ra Chence S. Spier E., Shon M., Walley K.,

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MEDLINE-22426065; PubMed=12537568;

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Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., Patel S., Adams R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeilfer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C. Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., Pinishing a whole-genome shotgun: release 3 of the Drosophila
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebbydroidea; Drosophilidae; Drosophila.
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Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                             'Annotation of the Drosophila melanogaster euchromatic genome:
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FlyBase; FBgn0003372; Sgs1.
SEQUENCE 1225 AA; 127735 MW; A99AF9D4404C79F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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Craniata, Vertebrata, Euteleostomi, Catarrhini, Hominidae, Homo.

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;

NCBI_TaxID=9606

sapiens (Human)

Homo

Proteoglycan 4 (Fragment).

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PKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPV 1058
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RESULT Q6DNC4

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REDIENCE FROM N.A.

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
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A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dockon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
A Durbin K.J., Evangelista C.C., Ferriaz C., Ferriera S., Fleischmann W.,
Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Jones A.R., Hughes C.E., Flannery C.R., Caterson B.;
Submitted (10N.2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY653038; AAT74746.1; -
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Matches 247; Conservative
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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.
RA Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
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RA Gibbs R.A., Mores E.W., Rubin G.M., Venter J.C.;
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT Griden Sequence of Drosophila melanogaster.";
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MEDLINE=2246070; PubMed=12537573;
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Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
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"The transposable elements of the Drosophila melanogaster euchromatin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A. Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Sacleb J.M., Park S., Feiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.B., Myers B.W., Glbbs R.A., Rubin G.M.; melanogaster euchromatic genome sequence."; of the Drosophila Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Annotation of the Drosophila melanogaster euchromatic genome:
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EMBL; AE003626; AAS64673.1;
InterPro; IPR011009; Kinase_like.
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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Gaps

18.6%; Score 1311.6; DB 2; Length 1761; 23.1%; Pred. No. 7e-19; ive 108; Mismatches 379; Indels 1044;

Conservative 108;

Similarity

Best Local Simi Matches 459;

1761 AA; 197521 MW; 62A5E16E6241B3F4 CRC64;

SEQUENCE Query Match Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Drosophila melanogaster (Fruit fly)

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TTKRTTAEMSTTNQEPTSVETTTNSSNQSNTTTESTTTEEQHVHHHHHHHHHYH---KPAD 1675
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RADILMES-20196005; bubmed=10731132;

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MEDLINE=22426065, PubMed=12537568;
Celniker S. E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A Patel S., Adams W. (Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Patelb J.W., Park S., Pfeiffer B.D., Richards S., Sodergren B.J., Solriskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.";
Genome Biol, 3:RESEARCH0079-RESEARCH0079(2002).
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                                Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila
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SEQUENCE FROM N.A.
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519 091 İTQKSİTLRITEBPTTRKSSTAKİTREPTTKRETTERTTKEPİTRKTİTHKİTEBPTTKK 1150 680 EPATKKTTHEPTTQKSTTLRITEEPTTRKSSTAKTTREPTTKRETTERTTKEPTTRKTTT 739 740 HKTIEEPTTKKTTHEPTTKKSTTLKPTEEPTTRKTSTTKTTREPTTKRKTTERTTKEPTT 799 300 RKTTTHKTTBEPTINK----TTTKKTTHEPTTKKSTTLKPTBEPTTRKTSTTKTTREPTT 855 -----PITPKKLT-----PIT-PEKLAPTT 543 577 KAAAPNTPKEPAPTTPKEPAPTTPKEPA-------PTTPKETA-----PTTPKG 618 619 TA-----PTILKEPAPTTPKKPAPKELA-----PTTTKEPTSTTSDKPA-----P 658 206 KITEEPTINKITIKKITHEPITKKSTILKPIEBPITRKISITKTITREPTTKRVITERITR 1265 325 TKRVITERITREPITRKTITHKITEEPITKKTITKKTIHEPITKKSTILKPIEEPITRKT 1384 856 KRETTERTTQEPSTSKTTTHETTAEPATKKTTHEPITQKSTTLRITEEPITRKSSTAKTT 915 544 PEKPAPTIPEBLAPTIPEEPT-----PIIPE---EPA-----PTTP 576 916 RĖ---РІТКRÈTTERITKEPITRKTTTHKITTEEPITKKTTHEPITKKSTTLKPTEEPITR 972 659 TIPKGTA-----PITPKEPAPTIPKEPA--------PITPKGTAPTILKEPA--- 697 563 TKKTTIKKTTHEPTTKKSTTL----KPTEEPTTKTSTIKTTREPTTRETSTSVKTTADQ 1618 519 TTKRITAEMSTINGEPISVETITINSSNQSNITIESTITEEQHVHHHHHHHHHHYH---KPAD 1675 ------PTTPK----KP----APTTPETPPPTTSEVSTPTTK 771 BP----TILHKSPDE----SIPELSAEPIPKALENSPKEPGVPTIKTPAATKPEMITT 821 887 984 -----TRPNQTPNSKLVEVNPKSEDAGGAEGETP------HMLLRPHV 1020 121 FMPEVTEDWDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWML 1080 981 SPFSPPSPARRITEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIF 1140 888 LAP-----KVTTTK-----KTITTEIMNKP------EETAKPKDRAINSKAIT 925 --PTTPKKPAPTTPKEPA-843 ---KMTKETAT---TTEKTIESKITATTIQVISTTIQDITPPKITTLKT-----TT 940 ------STKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTT---698 ----PTTPK----KPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPA---------PTTPKEPAPTTTKKPA--PTAPK-----EPA---926 PKPQ-----KP------TKAPKKPT----------EPA-----EPA-------1688 -PLPLPLP-----WP-PLPLPEI----576 LGPSILP----LPDLP-----520 PKETA-----822 AKDKTTERDLR------772

	33
Qy 1141 KGFGGLTGQIVAALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCFGKKFALNIFVI 1200 nh 1708PDLPTA	575
1201 GEMTQVRRRFERAIGPSQTHTIRIQYSPARLAYQDKGVLHNEVKVSILWH	
Db 1726LPEVNLTA 1733	Qy 369 TTPKEPAPTTKEPAP TTPKEPAPT 392
Oy 1261 ISLPNIRKPD 1270	Db 694 PEPSTTPGTTRITPTRPISTESTDTIMSSASTPEPSTTRTTPTRPISTESTDTIMS 753
Db 1734 ISLPEISLPN 1743	
RESULT 12	TDTTM
Σ	
Q7PMD5; 01-MAR-2004	TTMSSASTPEPSTTPGTTRTTPTRPTSTEST
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update) DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
ENSANGP00000 Name=ENSANGC	TTMSSASTPEPSTTPGTTRTTPTRPTSTES
Anopheles gambiae str. PEST. Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,	
	Db 994 STESTDTTMSSASTPEPSTKPGTTRTTPTRPTTPTTBTTMSSASTTEPSTTPGTTRTTP 1053
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.	Qy 510 TAPKEPAPTTPKETAPTTFKKLTPT
	Db 1054 TRPTSTESTDTTMSSASTPEPSTTPGTTRTPTRPTSTESTDTTMSSASTPEPSTTPGTT 1113
DR EMBL; AAAB01008980; EAA13969.2; DR GO: GO: 016020; C:membrane; IEA.	Qy 538 KLAPTTPBTPB
	Db 1114 RITPIRFISIESIDTIMSSASTPEPSITPGITRITPIRPISIESIDTIMSSASIPEPSIT 1173
NON_TER 1 1 1 NON_TER 3150 3150	TESTDTTMSSASTPE
SEQUENCE 3150 AA; 322879 MW; 3C/B3D441CE8C839 C	
atch 18.0%; Score 12/1.2; UB 2; Length cal Similarity 19.0%; Pred. No. 1.55-17;	PSTTPGTTRTTPTRPTSTDTTMSSASTPEPSTTPGTTRTTPTRPTSTESTDTTWSSASTP
Matches 447; Conservative 120; mismarches 155; indices 1510; c.e.	
TPTRPTPTDSTMSSASTPEPSTTRTTPTRPTSTESTDTTMSSAST	
	1352 SSASTPEPSTITPGTIRITPTRPISIESTDTIMSS
DD 276 PEPSTTPGTTRTTPTRPTSTESTDTTMSSASTPEPSTTPGTTRTTPTRPTSTESTDTTMS 335	652
	1412 DIT
H	Qy 678TIPK 702
	Db 1472 TESTDTTMSSASTPEPSTTPGTTRTFTRPTRFTSTESTDTTMSSAYTPDPSGIPGTTRTTPT 1531
MSSASTPEPSTTPGTTRTTPTRPTSTESTDTTMSSASTPEPSTTPGTTRTTPTRFTSTES	
260TTPKEPASTTPKEPASTPKEP	TMSSASTPEPSTTPGTTRTTP
455 TDTTLSSASTPEPS	
274KERA-FIIIKSAPITEKERA-FIIIKSAFIIK	TIMSSASIPEPSTIPGTIRITPIRPISIESIDITMSSASIPEPSTIPGIT
	Qy 735 PTTPKEPAPTTPKKPAPTTPETPP 758

Lau J.,

Chlamydomonas reinhardtii. Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas. NCBI_TaxID=3055;

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78;
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50 LAWVTIPVSDALQFPVNVSVTSSAATDAPSAIAYIGALLDVLWNVPWQPNCINDTRRSYD 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 17.2%; Score 1211.6; DB 2; Length 3409; Best Local Similarity 13.7%; Pred. No. 3.2e-16; Matches 384; Conservative 167; Mismatches 447; Indels 1814; Gaps
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                                                                                                  P SEQUENCE FROM N.A.
A PETIS P. D., Waffenschmidt S., Umen J.G., Ishida K., Kubo T., Lau B. Scodenough U.W.
L Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
BMBL, AY$15930; AA$07044.1; -.
DR INTEFPO; IPR003882; Pistil extensin.
DR PRINTS; PR01222; ATROPHIN.
DR PRINTS; PR01218; PSTLEXTENDIN.
DR PRINTS; PR01218; ASTLEXTENDIN.
SQ SEQUENCE 3409 AA; 336045 MW; 7FE87633EDD6631F CRC64;
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---TPKE 357

GeSSE6;
CJUL-2004 (TrEMBLrel. 27, Created)
O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
O5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Plus agglutinin.
Name=SAG1;

PRT; 3409 AA

PRELIMINARY;

Q6SSE6 RESULT 13 Q6SSE6 ID Q6SSE AC Q6SSE DT 05-JU DT 05-JU DT 05-JU DE PLUS GN Name=

7		дū	1771 TTTLVAAASSSFAQAIRAKGSLLQGSYHLQN
a ò	APTIKEPAPTIPKEPAPTAPKKPAPTIPKEPAPTTFKEP	δy t	894TTKKIIITTE
2 AG		g À	1831 VAGNIGEABAAMEINBABATAABAGAAX
δλ	414 APTTYKEPSPITPKEPAPTITKSAPTITKEP 444	qa	. :   ::  1 SP-PRRPPPPAAGSTGLLFSNAD
g &		\documents	943 KPKTMPRVRKPKTTPTPRKMTSTMPELN-
e do	:	3 &	TTRPNOTPNSKL
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qq	TPPSPVPPSPAPPSPAPPSPAPPSPAPPSPAPPSPAPPSP	λ̈	1002 EDAGGAEGETPHMLLRPHVFMPEVTPDMDY1
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δλ		qu	:   2175 GGAASGACADVGAMAAPATVAAGADVPSED
qa		ò	1145 GLTGQIVAALSTAKYKNWPESVYFFKRGGS
δλ	TLKBPAPTTPKKPAPKELAPT-TTKGPTSTTSDKPAPTTPKETAPTT 73	đ	2230 GSGGGWVPL
Пр		ò	1199VYGEMTQVRR
δλ		q	2261 GAATAAGGGAATAPGSPRGAAAGE
qq	PSPAPPLPVPPASPAPSPSPL	λō	1239 VLHNEVKVSILWR
٥x		qa	2292HWRKFSVPDDGAATAGVGVD
Dp	1358 RPPQPQTPAMPPPSPAPPSPAPPSPAPPGVPPPPPTPPLAPLPPDCTLLAQAALLSIP 1417	ð	1252
δŏ		qa	2342 PSDDGAKGRSSSHGGGNGGNAMSSGAASFG
Ωp		ζŏ	1259 SAISL
δλ		qu	2402 SGAAMRGGGAGASRFGPAGSRAGSPPEGAG
qo	1478 GNYYSNGGDAAIQRIFAGNSTDRGGSSSGSGSGSSSWGPGTETAAEWAVDAVQDGTYQLQL 1537	λο	1264PN
δλ	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	qa	2462 GSGSNEGGSRQMSYGSNNAMTAGAVGVGGC
qa	LTISFSE	ζ	1288 PSRTARAI
δλ	ETTTAAPKWTKETATTESKIT	qq	2508 PPPLPAPGTVPLPFANLLTSGADVRSRRAI
qq	1598 PVPAFDPAASLIVTGALVAEWVAAADKMTFYVLAMTLPAELVATAAGSSSSSGTSKSGNG 1657		
δ		RESUL' AASO7	
qq		A ID	044 PRELIMINARY; PK1; 34 044;
λ	DTTPFKITTLK	DT 02-MA	02-MAR-2004 (TrEMBLrel. 27, Created) 02-MAR-2004 (TrEMBLrel. 27, Last sequel
Dp	1718 PATAYADAARNPGRNDLSLSVELTDNAVASPAVGEALATTARVTAATYPAVAA 1770	1 B 6	k-zoot (iramantei. 277) agglutinin.
δλ	885 TTTLAPKVT 893	OS CEN	ondi. Chlamydomonas reinhardtii.
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1263 PNIRKP-----DGYDYYAFSKDQYYNIDV 1287 :|:| GGVRRPAGSLRNASDG-----DA 2507 1258 1258 | | :: FGASAGGGGAAAASKLGSRSGSPGDGDYNAMS 2401 DSQY----WR-FINDIKDAGYPKDIFKGFG 1144 RRRFERAIGPSQTHTIRIQYSPARLAYQDKG 1238 AGGYAGGANAMFAGTAGRAGAISPAHDGSSRP 2461 -FPRLE----- 2064 ----YFWMLSPESPPSPA 1089 : | |: SRTAAYCVLTIAVVPYAAFLWWLA----- 2116 VFTRCN----- 1110 SIQQYIYKQEPVQKCPGRRPALNYP----- 1198 ------PPLVALPGSGRHLPLPPLLPAA 2260 |:|: TLVVAAMLITAVAAGRLIAAVLYRLLVSPE- 2053 YLPRVPNQGIIINPMLSDETNICNGKPVDGL 1061 AFERADRISPRESTVSIATAADIGGTATGGG 2174 QMLTMSLYLASRGVGREYGEYAVEFKYAVLG 1830 3DLWPIGNDLLGGSSNTTASGSSSGSSSSSN 1890 LAVATPALPAPLPSTIAAAATAAP----- 1942 : HIMQQMLQPPAAAVAAPPPPPASSSALVLQP 1994 -----TKAPKKPTSTK 942 N-----PTSRIAEAMLOT 982 -----IMNKPEETAKPKDRATNSKAT 924 AI----TTRSG 1300 |: | SINAEAVAAAAGGGGGGGGTSRSG 2559

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768	414	828	445	888	490	947	526	1007	569	1066	619	1126	643 7	1186	679 E	1245 E	738 F	1298 F	797 E	1358 R	812 -	1418 D	823 -	1478 G	832 -	1538 S	836 -	1598 P	862 -	1658 NC	862	1718 PA	885 TT	1771 TT	894
qq	QY	Ωp	δ	qa	δλ	qq	ζŏ	Db	δy	ΩÞ	λ	qq	δy	qa	δλ	qq	ζ	QΩ	ζŏ	qa	ò	qq	δλ	qq	ò	Ор	δ	qq	δλ	qa	δλ	qq	ò	<del>Q</del>	ò
<pre>Bukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas. NCBI_TaxID=3055;</pre>			"Flus and Minus Sexual Agglutinins from Chlamydomonas reinhardtii."; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.		Query Match 17.2%; Score 1211.6; DB 2; Length 3409;	tches 384; Conservat	1 MAWKTLPIYLLLLSV	:   : : 50 LAWVIIPVSDALQFPVNVSVISSAATDAPSAIAYIGALLDVLWNVPWQPNCINDTRRSYD	17	110 APWPSRCALPAVQYGYYDETYIDATVYSGNSLRPFYSTCRYPASSDPYAFLEPYSMPWVD	17PVIQQVSSQDLSSCAGRCGEGYSRD	170 DFGIYQPVLDGFDMWWGFTVNTVDSNLKWIDPAWTAQGAWLGGQDFRD	42 ATCNCDYNCQHYMECCPDFKRVCTAELSCKGRCFESFERGRECDCDAQCKKYD 94	218 AVMNFGTHYCSWPFVECSSCENYDIA	76	244 DPYDPDKIANGIVPAVITALDFRNASLYIYYLDFGMFPAGSLDNVWYLNLAYNFIGGPLP	95YESFCABXCCPDYESFCAB	304 ANLPTILPSLQHLALDHCRATPDVRGTASLQYGWQQYPSTGQPYE-YCSDGDVTGSDGTE 362	107 106	363 YVISGMIPDEWGDAVAAAASDSSLPWANIRTVRLSNQALYGPIPEGIRSASSSISSWRLQ 422		GECLAPPPPSPSPRPP		483 RPPPLPPSPPPLLPPSPPVPPPSPPSPPSPPSPPSPPBPSPPLPPSPPLPPSPPSPPSPTPVARCIOV 542			146STIQHNKVSTSPKITTAKPINPRPSLPPNSDISKETSLIVNKETIVETKETITINKO 202		203 TSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTP 262		263 KEPASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTT 315			708 PSPEPPSPAPPSPAPPSPAPPSPAPPSPAPPSPEPPSPAPPSPEPPSPAPPSPAPPS 767	358 PAPTTPKEPTPTTFKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEP 413
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GLP----NVVT 1258
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1831 VKGNLGPABAAMPTNEKEVTAAEQARQVGGDLWPIGNDLLGGSSSNTTASGSSSGSSSSSN 1890
                                                                                                                                                                                                                                                        -----PRLPSP----PPPAVGSSTGVLPRRHLMQQMLQPPAAAAVAAPPPPASSSALVLQP 1994
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| SPPPPPPSQLLIQQASATYVSDMQDLLYTLVVAAMLITAVAAGRLIAAVLYRLLVSPE-
                                                                                                                            1891 SP-PRRPPPPAAGSTGLLFSNADASPPPLAVATPALPAPLPSTIAAAATAAP-----
                                                                                                                                                                                               ---PTSRIAEAMLQT
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 Jones A.R., Hughes C.E., Flannery C.R., Caterson B.; Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases. EMBL; AYS36119; AAS3377.1; -. Interproj. 1PR 1000585; Hemopexin. Pfam; PF000120; HX; 2. SMART; SM00120; HX; 2. NON TER 251 251 251
                                                                                                                        28532 MW; 2011B2C1719AA68B CRC64;
                                                                                                                                             16.7%; Score 1183; DB 2;
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sive 10; Mismatches 22;
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Matches 218; Conservative
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                                                                                                                            SEQUENCE
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AC Q6QUE3;
DT 05-UL-2004 (TrEMBLrel. 27, Created)
DT 05-UL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-UL-2004 (TrEMBLrel. 27, Last annotation update)
DT 05-UL-2004 (TremBLrel. 27, Last annotation update)
DF Proteoglycan 4 (Fragment).
DF Proteoglycan Bovine).
CS Bos taurus (Bovine).
CS Bostaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
CS Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Bovidae;
CS Bovinae; Bos.
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CS Bovinae; Bos.

RESULT 15

seq1-h.rpr

## GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

October 13, 2004, 11:23:49; Search time 26.7037 Seconds (without alignments) 4723.689 Million cell updates/sec

SEQ1-H Title: Perfect score:

1 MAWKTLPIYLLLLSVFVIQ......ARAITTRSGQTLSKVWYNCP 1311 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.1

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 1264

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

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qa	λō	QQ	79	QQ	δλ	Ωp	δ	Db	δ	qq	ζ	Dp	δλ	Ωp	δλ	Ωp	Qy	Ωp	٥'n	qa	δ	QΩ	λ	q _C	δy	Db	δλ	qq	δ	qq	RESULT T18262 S-layer C,Speci C,Date: C,Ate: C,Fujin J. Bact A,Title

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A;Accession: T18262
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Atacule type: DNA
A;Residues: 1-1664 <FUJ>
A;Residues: 1-1664 <FUJ>
A;Cross-references: UNIPROT:Q06852; EMBL:X67506; NID:9296879; PID:9296881; PIDN:CAA4784.
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                                                                                                        Query Match
16.3%; Score 1154.2; DB 2; Length 1664;
Best Local Similarity 20.5%; Pred. No. 7e-17;
Matches 404; Conservative 135; Mismatches 417; Indels 1018;
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A, Reference number: Z18847; MUID:93209931; PMID:8458832
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10.000			C;Acces R;Labei Science	8810n: 138348 L. S.; Kolmerer, B. 270, 293-296, 1995
5.29 KKLTPTTPEKLAPTTPEKRAPT-TPEBLAPTTPESPTPTTPESPAPTTPE  9.20 DEPPSDEPTSPET  10.5 SOETPSDEPTSPET  10.5 SOETPSDEPTSPET  10.5 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SOETPSDEPTSPET  10.6 SO			A, Title A, Refer A, Acces	3: Titins: giant proteins in charge of muscle ultrastructure and elasticity. rence number: A57430; MUID:96026330; PMID:7569978 ssion: 13846.
1016 SEPTEMBERPEP - PEKERAPTPEKERAPTTPKGTAPTTEKERAPT-TP 632  1016 SEPTEMBERPERSEPERPEPTENDERSEPPERSEPTES PERPERPERPERPERPERPEPTE 1034  1019 SEPTEMBERPTERSEPTES PROBERPES			A;Statu A;Molec A;Resid A;Cross	Ns: preliminary; cramstanced from CD, Erby, DECO. Thus: 1-7962 <res> sylves: 1-7962 <res> sylves: 1-7962 (NIPROT:Q10465; EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g101</res></res>
1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Property   1.00   Pro			C;Genet A;Gene: A;Cross A;Map F	lucs: DEB:TIN 5-references: GDB:127867; OMIM:188840 Sosition: 2q31-2q31
11.0			Query Best Match	14.7%; Score 1038; DB 2; Length 7962; Similarity 13.0%; Pred. No. 7e-13; 3; Conservative 129; Mismatches 466; Indels 2360; Gaps
13   ENGINEERING	APTILKEPAPTIPKKPA	73	ob ov	QQVSSQDLSSCAGRCGEGYSRDATCNC
112   PHRALENSPRICEPOPTRICEPARTICAL PORTRETTA 650   07   15   15   15   15   15   15   15   1		79	čo qa	
112   FORTH SENTIAL PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY TO THE PROPERTY		85 13	da da	ESFERGRECDCDAQCKKYDKCCPDYESFCAEVKDNK
123   PHYPORATHORACHER   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERTIES   PARKED STRICK PROPERT		91	\dot{\text{q}}	KNRTKKKPTPK
133   134   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135   135		96 PTSGS 13	Qy	PPVVDESG
1007 AGGETPHRALREPHYENDEVENDELTRINNICARPUDGITTHEN 1066 Db 5117 GRIFFSTELTUNKEIT 1067 GTLVAPRGHPRATE 1067 GTLVAPRGHPRATE 1067 GTLVAPRGHPRATE 1067 GTLVAPRGHPRATE 1067 GTLVAPRGHPRATE 1067 GTLVAPRGHPRATE 1067 GTLVAPRGHPRATE 1067 GTLVAPRGHPRATE 1067 GTLVAPRGHPRATE 1067 GTLVAPRGHPRATE 1067 GTLVAPRGHPRATE 1067 GTLVAPRGHPRATE 1067 GTLVAPRGHPRATE 1067 GTLVAPRGHPRATE 1067 GTLVAPRGHPRATE 1067 GTLVAPRGHPRATE 1067 GTLVAPRGHPRATE 1067 GTLVAPRGHPRATE 1067 GTLVAPRGHPRATE 1068 VAROASASPYSDLANTSTATT 1068 VAROASASPYSDLANTSTATT 1068 VAROASASPYSDLANTSTATT 1068 VAROASASPYSDLANTSTATT 1069 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1060 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRATE 1070 GTLVAPRGHPRAT			VQ da	LDNGDFKVITPDISTIQHNKVSISEKITTAKPINPRESLPPNSD
1067 GTLVAPEGHYFWMLSPFSPRARITEVWGIPSPIDTVFTRCNCEGKTFFFKDSQ 1122   1		3111NPMLSDETNICNGKPVDGLTTLRN 1066             	Qy	
123 Y		11	ζΟ Α	
148GQ-IVAALSTAKYKN		11	중 유	GBEEEIDIMELLKNVDPKEYEKYARMYGITDFRGLLQAFELLKQ
17.9   IYKQEPVQKCPGRRPALNYPVYGEMTQVRRRFFERALGPSQTHTIRIQYSPARLAYQDKG 1238		11	o da	
234		12	o da	
Qy 234	VLHNEVKVSILWRGLPNVVTSA	DIMDGALDHSYIIE	Oy Dp	
			۷۷ ط	234 233 5477 GOYTCKYEDLETSAELRIEAEPIQFTKRIQNIVVSEHQSATFECEVSFDDAIVTWYKGPT 5536

Db   1089 PGGVTAVPPEISLPPKETPQNATPNESLAASSQKRSPKTSVPKETPPGGVTAMPLEIPSA 1148	486 TTPKEPAPTTPKKPAPTAPKE-PAPTTPKETAPTTPKKTTPTTP  1327 KTAVPKETSAPSECVTAVPLEIPPSPRKAPKTAAPKE-PAPTTPKKTTPTTP  1327 KTAVPKETSAPSECVTAVPLEIPPSPRKAPKTAAPKETPAPSPEGATTAPVGI-PPSP  537 EKLAPTTPEKPAPTTPEELAPTTPEEPAPTTPKAAAP	1		Db 1702 ETSETSV Qy 900 TTTEIMNKPEET Db 1753DSH Qy 936 Db 1802 APIQKSPGANSN	QY   975   IBEAMLOTTTRPNQ
RESULT 5 T30826 nascent polypeptide-associated complex alpha chain, muscle splice form gp220 N/Alternate names: alpha-NAC protein C;Species: Mus musculus (house mouse) C;Dacte: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004 C;Accession: T30826 R;Yotov, W.V.; St-Arnaud, R. Genes Dev. 10, 1763-1772, 1996 A;Title: Differential splicing-in of a proline-rich exon converts alphaNAC in A;Reference number: Z20889; MUID:96312450; PMID:8698236 A;Accession: T30826 A;Accession: T30826 A;Accession: T30826	EMBL:U48363; NID:gl666688; PID:gl66 (0/3; 2099/3; 2142/3; 2183/3 ts alphanAC into a tissue-specific The binding; transcription factor ore 1021.4; DB 2; Length 2187; ed. No. 9.6e-14;	vative 159; Mismatches 479; Indels 896; Gaps	80 RGRECDCDAQCKKYDKCC	RQGHPDASVTAKGTVVCLADSSLDTSVSASKGSALSGASSPLYPLEVSFLPEAGLAVQGPNKVSTSPKITTAKPINPRBSLPPNSDTSKETSLTVNKETTVETKE KGSLNKLSPTPPSSKGAPV-PSTGAPPSPKGPTVPTESSISSKQVPAEILPSPQK	TTTKG SLKGA KEPTP KGP-P PTTTK  :: ATSS PKE      PKETP

	12
8 8 8 8 8 8	8 4 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6
OY 1196 NYPVYGEMTQVRRRFERALGPSQTHTIRIQYSPARLAYQDKGVLHNEVKVSILW 1250  1	RESULT 6  The general control of the coldic repeat protein precursor - Phytophthora infestans Class of General Coldic and Coldic at the bight agent) Class of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile of Carcession - Tile o

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Qy 1188	CPGRRPALMYPVYGEMTQVRRRRFERAIGPSQTHTIRIQYSPARLAYQDKGVLHNEVKVS :     :	Db 459 KTPVLKRKEPAAKDTAKPATSKTPETPEKKDPVKPRDSSPKKVAAKPDSAQAPATPVKNP 518  Qy 500 ATPK 521
Db 1478	78	Db 519 VKKWRPPWEDDETPADDVSKPTDAKKTPSLAKKDPAPAKESLKPKADTKAPAKPRDPSPK 578
	ILWRGLPNVVT	QY 522 ETAPTTPKKLTPTTPBKLAPTTPEKPAPTTPEELAPTT 559
Db 1485	35NVVT 1488	Db 579 KVAPTAPEKKTPVLAKKEPAGPADSKTKEPEKSKPRDPSPKKAVPAKPVPKTEVAPAA 636
RESULT 7		560 PEEPTPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPA
hypothetical	hypotherical protein F35A5.1 - Caenorhabditis elegans C. Species: Caenorhabditis elegans	KAEPNSPVVP-PTPVKNPVKKWKPPWEDDDAPAKPVSLPEPE
C;Date: 20-Sep- C;Accession: T1	20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004 sion: T16251	605
R;Leimbach, submitted to	D. o the EMBL Data Library, January 1996	694 KKTPVLAKKAPTKEDSEAAADPVSGESSKDFKLAKKAFVKFKDFSFURAVFIAFFKIEV
A;Descriptic A;Reference	A; Description: The sequence of C. elegans cosmid F35A5. A; Reference number: Z18485	OY 641 APTITK-EPISTISDKPAPITENGIAPITE-ARF
A;Accession: A;Status: pr	A,Accession: 116251 A,Status: preliminary; translated from GB/EMBL/DDBJ	
A;Molecule t A;Residues: A:Cross-refe	7: EMBL:[	VPEPEKKTPVLAKKTPVKPRDPSPKKAVPAKPSTKTDAPPVSVKKPEPVSKPKEPSPKKA
A; Experiment		Qy 709LAPITIKGPISITSDKPAPITPKETAPI-TPKEPAP 743
A; Gene: CESP: F35A A; Map position: X	CESP:F35A5.1 Ssition: X	972 BPNSPVVPPTPVKNPVKWKPPWEDDDEPTEEVKKPSEPEKKTPVLAKKEPEKPKDAPKV
A; introns:	24.28	
Query March Best Local : Matches 34	Similarity 22.9%; Pred. No. 5.16-14; Conservative 106; Mismatches 332; Indels	932 AAKPRDPSPKKAVPEKEPAKVAAKPRDLSPKKAIPIPANTQEAPPTPVKNPVKKWKPPWE
Qy 11	KPPVVDBAGSGLDNGDFKVTTPDTSTIQHNKVSTSPKITTAKP 16	Cy 781 DESTPELSAEPTPRALENSKEPGYFTTK-TPATKFEMITIAKUKITEK 829
qq	3 SRAPPTPIKNPAKKWKPPWESVDE25	830
Qy 16	TQSIEKTS	1037
Db	STPAPSKLEKKPSLKR	Qy 871 TIQDTTPFKITTLKTTTTAKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQK 930
	AKDLAPTSKVLAKPTPKAKEPTPKEPTPKEPTPKEPTPKEPTPKEPTPKEPTP	Db 1076KTPVLAKKAPTKPATKPDSBAADPVSGPTSKDPKLSKKAPVEKP-K 1121
	-KD-APTKPVPSPGAPSPVPIKNPVKKMKAPWEDDEFMEEAPAAFVPAKKVKDFSPK	Cy 931 PIKAPKKPISIKKPKIMPRVRKPKTIPIPRKMISIM 966
	260 TTPKEPASTTPKEPTPTTIKSAFILE ZB5	
		DAGGAEGETPHMLL 101
S of	AKKTPVLKKKEPAAAAKPRDPSPKKAAPSKEHDPIVPPTPIKNPAKKWKPWEDDEVPTE	1182 DPLGGPKTKDPKLNKKAPAEKPTEKPKPKEVSKEPPK121
	P-KEPAPTITKEPA	1017 RPHVFMPEVTPDMDYLPRVPNQGIIINPMLS
Db 23	225 BIKBPBEPATRKVPALKKKEPSTSVKPVSDPSPTKKVPVKKEPEVPPTPIKNPTK 278	KTFFFKDSQYWRFTNDI 113
	368	1235 -WEDDPDEPE
	KWKPPWEDETPVEEVKEPPVPEKKAPVLKKKDPAPAAKARDPSFSKAAPKKVEPSSPVVP 33	OY 1131 KDAGYPKP 1138
Oy 40	403KEPA YEPA YTPKEPAPTIKKESFITEKEA 430 339 PTPVKNPVKKYKPPWEVDDEPAEEVKKPSAPEKKTPVLKRKEPERSSITESSDPSPKKAA 398	Db 1264GGPKP 1268
		RESULT 8
Dp 33	: :       : :	Jisto 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae) N;Alternate names: extracellular glucoamylase; mucin-like protein MUC1; protein XIR019c
Qy 4.	457KEPSPTTTKEPAPT-TPKEPAPTTPKKPAPTTPKEPAPTTP-KEP 499	C;Species: Saccharomyces cerevisiae C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

236 AKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTP  268 TKEKPTPPTTTSCTKEKPTPHHDTTPCTKKKTTTSKTCTKKTTTPVPTPSSSTTE  286 KEPAPTTTKSAPTTPKEPAPTTFKEPAPTTTKEPAPTTTKSAPTPKE  324 SSSAPVPTPSSSTTESSSAPVTSSTTESSSAPVPTPSSSTTESSSAPVTSSTTESS  342 PAPTTPKKPAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAP	451 SAPTTPREPSPTTTKEPAPTTP	905 VPTTKTPAATKPEMTTTAKDKTTERDLRTTAAPRKMTKE 847
8997; PID:g763364; GS on of STA1.	A, Molecule type: DNA A, Residues: 762-131 c'42> A, Molecule type: DNA A, Residues: 762-131 c'42> A, Molecule type: DNA A, Residues: 762-131 c'42> A, Molecule type: DNA A, Residues: 762-131 c'42> B, Pardo, J. M.; Janez, E.; Zalacain, M.; Claros, M.G.; Jümenez, A. FEBS Lett. 239, 179-184; 1989 A, Title: Similar short elements in the 5' regions of the STA2 and SGA genes from Sacchar A, Reference number: S27281, MUD: 89031230; PMID: 3141213 A, Molecule type: DNA A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Residues: 1.31 c, PAR> A, Cross-references: GB: U30626; NID: 91304386; PIDN: AAC49609.1; PID: 91304387 A, Cross-references: MIPS: Yeast glucan 1, 4-alpha-glucosidase homolog; glucan 1, 4-alpha-glucosidase C, Reportanily: Yeast glucan 1, 4-alpha-glucosidase homolog; glucan 1, 4-alpha-glucosidase C, Keyvords: glycosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosidase; hydrosida	## Similarity 22.8%; Score 956.2; DB 1; Length 1367;  Similarity 22.8%; Pred. No. 8.8e-13;  Similarity 22.8%; Pred. No. 8.8e-13;  Similarity 22.8%; Pred. No. 8.8e-13;  Lisvevique 113; Mismatches 512; Indels 638; Gaps 69;  Lisvevidue 113; Mismatches 512; Indels 638; Gaps 69;  Lisvevidue 113; Mismatches 512; Indels 638; Gaps 69;  Lisvevidue 113; Mismatches 512; Indels 638; Gaps 69;  Lisvevidue 113; Mismatches 512; Indels 638; Gaps 69;  Conservative 113; Mismatches 512; Indels 638; Gaps 69;  Conservative 113; Mismatches 512; Indels 638; Gaps 69;  Conservative 113; Mismatches 512; Indels 638; Gaps 69;  Conservative 113; Mismatches 512; Indels 638; Gaps 69;  Conservative 113; Mismatches 69;  Conservative 114; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mismatches 612; Mism
C;Accession: S48478; A26877; B26877 B,Rowley, K.  submitted to the EMBL Data Library, A;Reference number: S48478 A;Accession: S48478 A;Molecule type: DNA A;Residues: 1-1367 < ROW, A;Crossreferences: UNIPROT: P08640; B;Yamashita, I.; NaXamura, M.; Fuku J; Bacteriol: 169, 2142-2149, 1987 A;Title: Gene fusion is a possible of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro	A,MACCES101: LADBY 7 A,MACCES101: LADBY 7 A,Residues: 762-1331 <ya2, 1-31="" 179-184,="" 1988="" 239,="" 762-1331="" <par="" <ya2,="" a,molecule="" a,rardo,="" a,residues:="" a;mceference="" a;mitle:="" a;mosidues:="" dna="" e.;="" elements="" febs="" ianaz,="" jm.;="" lett.="" muid="" number:="" s27281;="" short="" similar="" type:="" zalaca=""> A;Cross-references: EMBL:X13857; R;Lambrechts, M.G.; Bauer, F.F.; Proc. Natl. Acad Sci. U.S.A. 93 A;Title: Muci, a mucin-like prott. A;Reference number: JC6123; MUID A;Reference number: JC6123; MUID A;Reference number: JC6123; MUID A;Reference number: JC6123; MUID A;Reference number: JC6123; MUID A;Reference number: JC6123; MUID A;Reference number: JC6123; MUID A;Reference number: JC6123; MUID A;Reference number: JC6123; MUID A;Reference number: JC6123; MUID A;Residues: 1-1367 &lt; LAM&gt; A;Cross-references: GB:U30626; NIC;Genetics: A;Map position: 9R C;Superfamily: yeast glucan 1,4-e;C;Superfamily: yeast glucan 1,4-e;C;Superfamil: transmembrane #telestences F;5-21/Domain: transmembrane</ya2,>	Query Match Best Local Similarity 22.8%; Pred. No. 8.8e- Matches 373; Conservative 113; Mismatches  QY   13 LLSVFVIQOVSQDLSSCAGRCGEGYSRDATC Db   6 LLAYLVLSILENSALGEPTALVPRGSSEGTSCNSI  QY   50

452 AECTDQAFSSDSSTISSHGADFTTTGEQIIEGSGSIQTSSGGSITVTRGLIPKDVELTTS 511	512 GRLACTSYCPPNSECVGGYCECVSGYGGNALVGCEDIDECITEICNIEANEWCVNLIGGF 571		VCCNPTNATHDDC1DFLTKVKIYAYM111FLLKGLE1TKEKGLHV1GGNEEDTVVATRSN		632 HSTSDQLITQVVQQSRNFSTGQIILTRGKVSSGBAVTQTTDADEFGLEISAADLAGSGSG 691	119PTPKPPVVDEAGSGL137  119PTPKPPVVDEAGSGL		- - - 750 GTIRVRITTLGEDGEPETATKPGISAPDKTGEGSKTESDGEEKLTVEKDGKEAQSSGSSA 809	149 148	810 ISSGKKSEATSGSSSSSAKSGTGSEASGSSGASSSSGSGVSGESGSSVSTESGSFGTSSS 869	149TTAKP 164	870 GSVGSEATGSTGVDGSESGKPSKSSTEEKLPFTKNGEKSPISGSDTTGKESSEETTSRKP 929	165 INPRPSLPPNSDTSKETSLTVNK	188 BITVETKETTIT	990 BITTDGEESSSTSTGDKSGGKPADKSDNKNVPKTGDKNPDITTDGEDSTSETSGGEQGPK 1049	223 TSAKDLAP 239	EEGSGILTTSSGGKN		1110 STFEHGTKLERLPPKTEDKSSETPQLGLEISAGKKPEPEDGTSKEVGLEILWESTTPGST 1169	 	270PKEPTPTTIKSAPTTPKEP 288	GETSGVDGK	289APTITKSAPITPKEPAPIT323	:  :: :	324TKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTT 362	1346 SGTEESTLPPTEGSGESTTSSAPTVEPATVLPPQNRNEKPEPTKDTFALPTTTTGAPQ 1403	363 365	1404 ANDSSVENTKCTSSDECGLDALCERRIGVCRCEPGFEGAPPKKSCVDVDECATGDHNCHE 1463		DGSCQDIDECTEHNSTCCGANAKCVNKPGTYSCECEN	368PTTPKEPAPTTK
d Qy	qq	ð	qu	Øy	qq	<b>&amp;</b> 45	łò	qa	λ	qu	δλ	QQ	රු සි	δλ	qq	λö	Ор	δ	d g	÷ €	3 8	i di	ò	qa	ò	qa	ζ	qa	Qy	qa	à d
OY 1142 GFGGLTGQIVAALSTAKYKNWPBSVYFFRGGSIQQYIYKQEP 1184	1185VQKC	Db 1268 TTYITTLIPGSNGAKNYETVATATNPISIKTTSQLATTASASSVAP 1313		Db 1314LQSAS 1328	Qy 1292 ARAITTRSGQTLSKVW 1307	Db 1329 GSAVATYSVPSISSTY 1344	RESULT 9		;)Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004 ;}Accession: T34513	ty Favello, A.; Vaudin, M. submitted to the EMBL Data Library, August 1994	4, Description: The sequence of C. elegans cosmid ZK783. 1, Reference number: Z21536	A,Accession: T34513 \Status: preliminary; translated from GB/EMBL/DDBJ	A,Molecule type: DNA A,Residues: 1-3507 <fav> A,Cross-references: UNIPROT:Q23587; EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN00021; CESP:ZK A.Experimental source: strain Bristol N2; clone ZK783</fav>	) Genetics: N. Gene: CESP: ZK783.1	A;nap position: 3 A;Introns: 14/1; 48/2; 84/1; 196/3; 303/1; 381/1; 586/1; 605/1; 1175/3; 1207/1; 1409/2;	3504/1	Query Match 13.5%; Score 951.7; DB 2; Length 3507; Best Local Similarity 12.7%; Pred, No. 8.79–12; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Cane 113; Versil Ca	Macches 454; Conservative 200; Mismarches 450; Mismars 2420; Cupo	:     :     :	Qy 31 AGR	Db 92 SGKGACLYDGAKPQCYCDSGFSGSACELQDKNECLEHPCHMMAQCQNTLGSYECRCLPGY 151		Db 152 BGNGHBCTDIDBCSDKLTSRCPEHSKCINLPGTYYCNCTQGFTPKGNQGSGLDKCADINE 211		2	84CDC	272 TIGGYECEEGFFEGDGKNCQRKCGHSVKLPSKSSCRKNSALCDRHASCHIVLDICDCKT	87	332 GYTGDGITCHDINECDAKDTPCSDGGKCLNLDGGYVCCKNGGDDAICLRDGGAFCSGGCG		110

Oct 13 12:38:28 2004	380 BPAP 383	1583 EDINECVAEKAPCSLNANCVNANGTFSCSCKQGYRGDGFMCTDINECDERHPCHPHAECT 1642	384 TTPKE 388	1643 NLEGSFKCECHSGFEGDGIKKCTNPLERSCEDVEKFCGRVDHVSCLSVRIXNGSLSSVCE 1702	389 390	1703 CEPGFRFEKESNSCVDIDECEESRNNCDPASAVCVNTEGSYRCECAEGYEGEGGVCTDID 1762	391PTAPK 395	TACTDEWSRLCE 18	40	1823 LEKKQCTVDEBEVPQCGACLPGHHPINGTCQSLQISGLCAQKNDCNKHAECIDIHPDSHF 1885	408TTP 410	1883 CSCPDGFIGDGMICDDVDECNNAGMCDDENTKCENTIGSFNCVCLEGFKKVDEKCVVDEK 1942	411 KEPAPTITKEPSPITPKEPAPTITKSAPTITKEPAPTITKSAPTITKSAPTITKSAPTITKS 458	1943 KQPNREKIEIDBENSSSSNSGQEKPTTKGIVSSTSATSSBSTTAEPHVTTSISSTTSTKD 2002	459 PSPTTTKEPAPTTPKEPAPTTPKKPAPTTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPT 518	2003 MISSKSPENVIMSSESPEVSTSSSKSTTASETTVSSTPSESSSSEAPLISSPA 2055	519 TPKETAPTTPKKLTPTTPE	2056 TITEVITESSVKSTIPKEESSSEITVKLSSKSPEVTESSVKSSPSIPSTISQSV 2109	564 IPITPEEPAPITPKAAAPNTPKEP611	2110 TSTVPETSKSTVLSSEAPVTSTSPTEVHTSSETKPSLSASSTTGDINSTTPSTSSLASVK 2169	612 APTTERGTTITKEPAPTTERKPAPKELAPTTTKEP 648	TSAPEGTSASVAPVKLSSLSPDV-SQPSTKTFDATESSTVQASETSSGTSVKST	Ţ	2229 HVTKLSITSSNPSSSVPVTSPKSTPTVPESTEQPTSTTPSGQSLTPMNSNSEVLTTSE 2286	688TAPTILKEPAPT-TPKKPAPKELAPTITKGPTST 720	2287 PHVLSSSLSPDVSQSSTTPNNLSBSSTVETPKTSSBVSLNSEBPSTTEAPTTLSPDILST 2346	721 T 730	2347 TINNLSQSSTVSTEDRSEISSENSEKPTSAPELVTSSVTHVASSSPDVPTESSEPDDLTG 2406	4TJ	2407 SSTENIPEASSKQTISSTPTPDTTTASEEPTKSTSMSPDLSTTSNVLSESSTTPESSSKS 2466	756TT9PPTTSEVSTPTTTT 775	2467 PVSSSTEGISVVTSTEFSKVPESTISSVLEEDLTKTPSPILEETTTASETSEPLTEDSL 2526	776IHKSPDESTPELSAEPTPKALENSP-KEPGVPTT 808	2527 TVSVRIHELTTSSENVPKESESTTTSSESSKPSQEPAGILTSTVVVPTSSVSLITASEIE 2586	809KTPAATKPEMTTTAKDKITERDLRTTPETTTAAPKWIKETA 849	2587 AITSNTPFKQGRTPITTSPKSLVKSTTSPSTVTSSEPSESTKRTTVSTTVSTTPFEETT 2646
Wed	δλ	ДQ	δλ	Op	ζ	qu	ζζ	QQ	δ	ΩÞ	δy	qa	Qy	DP	δ	Db	δλ	Dp	δχ	qq	δλ	DP	δλ	Dp	٥'n	qa	δ	qq	δγ	qq	δγ	qq	٥٧	qq	٥y	qa

Qy	850	TTTEKTTESKITATTTQVTSTTTQDTTPF 878
qa	2647	:-  TSESLILTAAPSKPTESTTESSEAPTTPAKTSETKPSNVSSTSRKSTENVETSTSQSGSL 2706
λõ	879	KITTLKTTTLAPKVTTTKKTITTT
DÞ	2707	: :   :           : : :         ESSTWSSTSSEPETNAPAVTVSSEASSTILEENSSTSSPTSSEASVKLSSLFPESITSEA 2766
δy	903	BIMNKPEB910
Dβ	2767	::            VIVSSRAPAEITMSSESHREISTVSSPREFIPLSTTVSPNVVTASSIPSEEPILSSVT 2826
Qy	911 -	TAKPKDTAKPKDRATNSKATTPKPQK 930
q ₀	2827 8	SSSTPRVRLITGTPDDLIVSVTVPSHGNRRQNITASSVPSNSTSPIILPSESLTTPQPPP 2886
ολ	931	TKAPKKPTSTKKPKTMPRVRKPKTTPTP
Ор	2887 T	
ζŏ	972 1	TSRIABAMLOTIT
QQ	2941 I	
δλ	- 586	RPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIIN 1043
qq	3001 K	KCDNSTRSCECBAGBAG
ò	1044 P	PMLSDETNICNGKPVDGLTTLRNGT 1068
ΩÞ	3024 P	
οy	1069 L	LVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTV-FTR 1108
ΩP	3084 T	TCKCNPGYFGNGLCCVPDPLDCVHFTGICHPNAVCNSESRQ 3124
70	1109 C	CNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTA 1157
DP	3125 C	
Qy	1158 K	KYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALN 1196
QQ	3153 -	::
č	1197 Y	YPVYGEMTQVRRRRFERAIGPSQT1220
QQ	3207 L	LCISGECICKSGFRRNSTLSGSETCADIDECAEKSHKCDRVATCRNTFGSHVCTCPDG 3264
٥'n	1221 -	HIRIQYSPARLAYQDKGVLHNEVKVŞILWRGL 1253
Db	3265 H	HVGDGITCVPHVNQGKLSVYCEADGMTLVLGNETADFEGKI 3305
٥٧	1254 -	PNVVTSAISLPNIRKP 1269
QQ	3306 F	FVKGQAENPYCSKSFSSLLNSRKPYVFKVVFQHCDVQLLDNHTWASTVVVQKHAMFLTNK 3365
ò	1270 -1	DGYDYYAFSKDQYYNID 1286
Db	3366 AI	
δλ	1287	VPSRIARAITTRSGQ 1301
Dp	3426 GI	GDTLKLALEVTPSENFGILPRNCFAINIESGE 3457

RESULT 10
T29757
protein UNC-89 - Caenorhabditis elegans
protein UNC-89 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Space: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Dec-1999
C;Accession: T29757
R;Du, Z.; Le, T.T.; Wilson, R.
submitted to the EMBL Data Library, May 1997

TTPKI	1614 E 1668 - 1668 - 1723 K 528 F	1 82 - ANTALDEVES FIRMENS PRIVED ANTEREAPTTER SERVETAPTTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEATTER SEA		Db 2188 LRWNLELDGPSPGTEVSWILNGQPLTKSDTVQVVDHGDGTYHVTIAEAKPEMSGTLTAKA 2247  Qy 699TTPK
d from GB/EMBL/DDBJ.  id from GB/EMBL/DDBJ  istol N2; clone C09D1  istol N2; clone C09D1  istol N2; clone C09D1  istol N2; clone C09D1  istol N2; clone C09D1	gt]	Db 777 PEIIWFINGKPLSESEKVKFISEDGICILTIKDVTRHFDGMYTCQGSNRLGSASC 831  Qy 87 DAQCKKYDKCCPDYESFCAEVKDNKKNRTKKKPTPKPPVUB	152	Db 1167 PLPTYEMSUNGRKVRDGQEGARVTRDESTUDGASILTIDTATYYSEVNHLTISVVAENTL 1226  QY 174

Db 3541 AKDEGSGHHTLTIKQARGEDVGVYTCKATNEAGEAKTTANMAVQEEIEAFLFVQGLK 3597  Qy 1082 PF-SPPSPARRITEVWGIPSPI	FGDVWSDVT	QY         1215	RESULT 11 S49915 extensin-like protein - maize c;Species: Zea mays (maize) C;Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004 C;Accession: S49915 C;Accession: S49915 R;Rubinstein, A.L.; Broadwater, A.H.; Lowrey, K.; Bedinger, P.A. submitted to the EMBL Data Library, June 1994 A;Description: Pex genes: pollen-specific genes with extensin-like domains.
TIKAESEEGVAE  WYIGTOLVCATE APTTET IPUSEETSLCDA TKEPTT TKEPTT	2728 VVCEAINEYGKATSEATLLVLPRGEPPDFLEMLSNVRARTGTKVVHKVVFTGDPKPSLTW 2787  779	TTTAAPKMTKETATTTEKT-TESKITATTTQVTSTTTQDTTPFKITTLKTTT  STATE STATE SKITATTTQVTSTTTQDTTPFKITTLKTTT  STATE STATE SKITATTQESITVESVEGVERVTITSSE	1028DMD
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B.Deference mimber. 940015	Db 821 APLSSPPLAPKSSPPHVVVSSPPPVVKSSPPAPVSSPPLTPKPASPPAHVSSPPEVVKP 880
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Db 17 LLLLAACLSACSVQAVTSAEASYIAHRQLLAMKEAGGGEAGDLPADFEFDDRVGAANFPN 76	
Qy 37GYSRDATCNCDYNCQHYMECCPDFKRVCTAEL 68	
nh 77 DRIBBAYTALGAMHRAFYSNDRGYTANWVGRDVCKYNGVICTEALDDPKITVVAGI 132	
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Db 249 VIVFANNAFVGCIPKSIGRMVKTLDEIIFLNNKLDGCLPLEMGLLVNTTVIDVSGNMLVG 308	
Qy 99 104	
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	RITEVWGIPSPIDIVFIRCNCEGKIFFFKD
	Db 1154SF 1164
	Qy 1121 SQYWRFTNDIKDAGYPKPIFKGF 1143
Qy 138 FKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETT 197	Db 1165NDIILPPIMANKYASPPPPPPPPPT 1188
Db 416PPSSPVPGKPAASAPMPSPHTPPDVSPEP 444	
Qy 198 TINKQISTDGKEKTTSAKETQSIEKTSAKDLAPISKVLAKPTPKAETTTKGPALTTPKEP 257	RESULT 12
Db 445	taracin-X - bovine
Qy 258 TPTTP-KEPASTTPKEPTPTIKSAPTTPKEPAPTTIKSAPT-TPK 301	C;Species: Bos primigenius taurus (cattle)
Db 474 TPPVPGKSPPATSPSPQVQPPAASTPPPSLVKLSPPQAPVGSPPPVKTTSPPAPIGSPS 533	C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-041-2004 C;Accession: T42629
302 врарттикврарттркврарттикврарттикварттур-кврарттрккрарттрккврар 360	R,Elefteriou, F.; Exposito, J.Y.; Garrone, R.; Lethias, C. J. Biol. Chem. 272, 22866-22874, 1997
534 PPPPVSVVSPPPPVKSPPPPAPACSPPPBKSPPPPRKSPPPPVKSPPPPPPPPPPPPPPPPPPPPPPPP	A,Title: Characterization of the bovine tenascin-X. A,Reference number: Z22180; MUID:97426436; PMID:9278449
361 ТТРКВРАРТТРКВРАРТТКЕРАРТТР-КЕРАРТАРККРАРТТРКЕРАРТТРКЕРАРТТТК	A, Accession: T42629 A, Status: preliminary; translated from GB/EMBL/DDBJ
594 PVKSPPPRARASPPPRAKSPPPRAKSPPPRAKSPPRAKSPPRAKSPPRAKSPPRAKSPPRAKSPPPREK	
	A;Cross-references: UNIPROT:018977; EMBL:Y11915; NID:g2462978; PIDN:CAA72671.1; PID:g246
OY 420 BESKITENERRYIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAKTIINSAK	C;Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin typ
473 YEADADTHEREDA ADTHOREDA	C;Keywords: extracellular matrix; glycoprotein; heptad repeat
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٥y	741PAPTTPKTAPTTPET 756
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δ	757 p 757
Db	2825 PLIGDLTVTGSSPDSLSLSWTVPQGHFDSFTIQYKGRDRPQVVRVGGEETEVTIGGLEPR 2884
٥y	791
qq	2885 HKYKMNLYGLHGGRRVGPVSTVGVTAPDYDAMTTQTPSTSVPEPPTKPRLGEV 2937
δ	792BNSPK
qq	2938 TVTDATPDSLSLSKTIPBEGQFDHFLVQYKNGDGQPKAVRVPGDBDGVTISGLEPDHKYKM 2997
٥٨	MTTTAKDKTTERDLRTTPETTTAAPKM   :
qq	2998 NLYGFHDHQRVGPVSVIĞVTTABEBTPSPTKMEETPSPTE 3037
ò	
ηq	3038 MEETPSPTEPSTEAPEPPEEPLIGELTVTGSSPDSLSLSWTVPQGHFDSFTVQYKGRDGP 3097
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Ωb	3098 QVVRVGGEETEVTVGGLEPGRKYKMHLYGLHGGRRVGPASTVGVTASLTTERPLAPRLGE 3157
δλ	869STTTODTT
Db	3158 LAVAVVĮSDTARLSWTVEQGPFDSFLVQYKDVQGQPQAVPVAGDLREVTVSSLAPGRKYK 3217
QY	891KUTLTKKIITTEIMNKPEETAKP
qq	3218 FLLFGLRDEKRHGPVSADAKTLPDTKPAPRLGELTVTDVTPGSVGLSWTV 3267
Qy	915ADRA 918
Dþ	3268 PEGEFDSFWVQYKDRDGQPRVVPVAADQREVTVPGLEPNRKYKFLLYGLYGRKRLGPISÅ 3327
δλ	919 TNSKATTPKPQKP 931
<b>q</b> 0	3328 EGSTAPLEKERQPPPRLGELTVTDETPNSLRLSWTVAQGRFDSFVVQXRGTDGQPRMVPV 3387
οy	932TKAPKKP 938
ΩÞ	3388 AADOREFIVEGLEPGRKYKFLLYGLLGGQRLGPASVLGMTAPEEDTPAPWHAATEAPKPP 3447
Š	939 938
qu	3448 EGPRLGVLAVRDVSPDSLRLSWSVVQGPFDSFVVQYQDTDGQPQALLVGGDQNKVLVSGL 3507
ò	939
qq	3508 EPSTSYEFFLYGLHEGKRLGFVSAEGTTGPVPAGQTPGEPGPRLSHLSVTDVTTSSLRLN 3567
ογ	939 971XKPKTMPRVRKPKTTPTPRKMTSTMPELNP 971
ΩD	3568 WEAPPEAFDSFLLRFGVPSPSTLEPQLRPLLQRELTVPGTRR-SAVLRDLHPGTLYTLTL 3626
λŏ	972TSRIAEAMLOTTTRPNOTPNSKLVEVNPKSE 1002
ПЪ	3627 YGLRGPHKADSIQGTARTLSPVLESPRDLQFSEIRETSARVSWTPPTSRVDGFKVSYQLA 3686
δ	1003 DAGGAEGETPHMLLRPHVFMFBVTPDMDXLPRVPNQGIIN 1043
DÞ	3687 DGGEPQSVQVDGRIQKLEGLIPGAQYEVIVVSVRGFEESEPLIGFLTIVPDG 3738
δλ	
qa	3739 PTHLRALNLTDESALLHWKPPQTPVDTYDVKVTAPGAPSLQASAPGSAVDYPLQGLVTHT 3798

4052 1181 KQEPVQKCPGRRPALNYPVYGEMTQVRRRRFERAIGPSQTHTIRIQYSPAKLAYQDKGVL 1240 3859 NIPGGQIQEIILPGGVTSHQLRGLFPSIPYSIWLRAMWGDSFIPPVSTSFITGGLRIPFP 3918 3919 RDCGEEMQNGVSTSRTTITELNGNRERPLNVFCDMETDGGGWLVFQRRMDGKTDFWRD-- 3976 1123 YWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNW--PESVYFFKRGGSIQQYIY 1180 3799 NYTATLRGLRGPNFTSPASITFTTGLEAPQDLEAKEVTPRTALLTWTAPEVSPTGYLLSF 3858 -----YSLRVD-----LRAGDEAVF 4021 1241 HNEVKVSILWRGLPNVVTSAISLPNIRKPDGYD-YYAFSKDQYYNIDVPSRTARA---1T ----YDSFQVDSADEYYRLHLEGYHGTAGDSMS GKTFFFKDSQ -WLGNEALHSLTKAGD----WMLSPFSPP--1297 TRSGQTLS------1310 4053 YHSGSVFSARDRDPNNLLISCAVSYRGAWWYRNC 4086 3977 -W-----EDYAH-----GFGNISGEF-TVFTRCNCE 1066 N--GTLVAFRGHYF -SPARRITEV----ID----I 4022 AQ-1087 1102 4007 g g  $\delta$ dC ð dd  $\delta$ g à qq ð ò

RESULT 13

proline-rich peptides 637K precursor, prostatic - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: 13-May-1992 #sequence revision 13-May-1992 #text_change 09-Jul-2004
C;Date: 13-May-1992 #sequence revision 13-May-1992 #text_change 09-Jul-2004
C;Accession: A42663; A41819; A31966; B20593; A20593
R;De Clercq, N.; Hemschoote, K.; Devos, A.; Peeters, B.; Heyns, W.; Rombauts, W.
J. Biol. Chem. 267, 9884-9894, 1992
A;Title: The 4.4-kilodalton proline-rich polypeptides of the rat ventral prostate are th

le exon. A,Reference number: A42663; MUID:92250652; PMID:1577819

A; Accession: A42663

A,Molecule type: DNA; mRNA A,Residues: 1-3706,'I',3708-4077,'F',4079-4155,'S',4157-5761 <DE2> A,Cross-references: UNIPROT:063455; GB:M86514

A; Experimental source: ventral prostate
A; Experimental source: ventral prostate
A; Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBID backbone (NCBIN:100347, NCBID:100348)
A;Note: sequence extracted from NCBID backbone (NCBIN:100347, NCBID:100348)
A;Declercq, N.; Hemschoote, K.; Devos, A.; Peeters, B.; Heyns, W.; Rombauts, W.
B;De Clercq, N.; Hemschoote, K.; Devos, A.; Peeters, B.; Heyns, W.; Rombauts, M.
A;Rocession: A41819
A;Accession: A41819
A;Rocession: A1819
A;Rocession: A1919-19165, Dirckx, L.; Claessens, F.; De Clercq, N.; Heyns, W.; Winn
B;Hemschoote, K.; Peeters, B.; Dirckx, L.; Claessens, F.; De Clercq, N.; Heyns, W.; Winn
B;Hemschoote, K.; Peeters, B.; Dirckx, L.; Claessens, F.; De Clercq, N.; Heyns, W.; Winn
B;Hemschoote, K.; Peeters, B.;
A;Rocession: A31966, MUID:89066721; PMID:3198617
A;Residues: 3372-5540 <+HEM>
A;Title: A single 12.5-kilobase androgen-regulated mRNA encoding multiple proline-rich A;Accession: A31966
A;Molecule type: mRNA
A;Residues: 3372-5540 <+HEM>
A;Residues: 3372-5540 <+HEM>
A;Cross-references: GB:MZ0721; GB:J04188; NID:6089733
A;Accession: B2053
A;Accession: B2053
A;Accession: B2053
A;Accession: B2053
A;Accession: A2063
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A;Accession: A2064
A;Accession: A2063
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A;Accession: A2063
A;Acc

Millone this peptide, designated proline-rich polypeptide IV, can be found at several lightness; this peptide, designated proline-rich peptides 637% precursor status absent with to introne subjected 6437 progrete; and the proline-rich peptides 637% proprotein astatus predicted 640% of the profited 640% of the profited forms of the profited 640% of the profited 640% of the profited forms of the profited 640% of the profited 640% of the profited forms of the profited 640% of the profited 640% of the profited forms of the profited 640% of the profited 640% of the profited forms of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited 640% of the profited	292	324A 343 1479 TDVTLPQQVSVQHLKPTEGIVQPLDLELTITPQPTPEGELSQTVQESTTQNKEPHKEVVA 1538	PTTPKK	350PAPTI 357 	358 -PAP 373     	374 373 1719 DHHKHINLTEVTNQPFHLEHTVQHQPTIEEERSQSIQKKTTQITEPGKKVVPLAQESEEV 1778	374PAPTTKEPAPTTP 386	387KE 388 1839 PNMEIELKHHGLFLLKTTEATTESENTNQMTKSLKQVTALFTQNKKSMLPALVESQDESQ 1898	389 PAPTAPKKP 408 	409TPKE 420	421 PSPTTPKEP 438 2018 PHGWIPHPPNTHGKIYLHYAEPPTGPFVEPPDLFFLKTTKSRPVEWTLTRTDKSRKEMVS 2077	439 444 2078 QSPKYBEAVLPVHGEGQEESRSPPNMSLQSLEQELTLSSQPHGWVPHPPNTHGKIYLHYA 2137	445 -APT	454TTP 456 2198 PSSPNMSLQSLDHELFMSSQPHGWIPHPPKTPDKIYLHYAEPPTGPFVEPPDLFFLRTTK 2257	457 KEPSPTTTKEPAPTTPREPAPTTP	TPKEBAPTTPKKEPAPKEP	23.1 V.P.HSGVPHPFKTPGKIYLHSIEPPPGPFVKPTDLILVKTTTKSKPAEWTPRRIDKLLKEM 23.76 516 APTTPK-ETA
Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   S	- MA	Qy	95 ab	₹ £	λζ da	λό da	QQ QQ	95 95	oy du	<del>ે</del> લ	ζζ 	QV Dp	δ da	Qy	<i>₹</i> 0 qq	ò f	75 ——
BABABABABABABABABABABABABABABABABABABA	us absent us absent copy gene with no introns copy gene with no introns copy gene with no introns copy gene with no introns copy gene with no introns copy gene with no introns copy gene with no introns copy gene with no introns copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gene copy gen	KTLPIXLLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQ	52HYMECCPDFKRVCTAELSCKGRCFESFERGRE	84CDCDAQCKKYDKCCPDYESFCAEVKDNKKRTKKKP	120	139	151INRVSISPKITTAKPINPRESLPNSD	177	193TROGE   194   1   1   1   1   1   1   1   1   1	EKTTSAKETOSIEKTSAKDLAPTSKVLAKPT	VTHIPAHKMTVPRQIQEDQGEYIISSNGSFQPLDLEVTLTSGIIPEVKHILPKRTVNPQT	YSQVKISHSQHVETQHPNSETTTVQPLDLEFAINLQPTPKENFAQTFQDTTTQMIGPPKE	VIAQAPEHHEGTIPIPIQDQAEYSTLPTVSFQPLDQELTITSEAIREPHPTVPQOTIIV	TPKE	TVVVGPVPIYEEVTVQTTSQDQAEYPESPTVSFOSLDIRITIRPRATRESVHDSLI.		IVNPPEHPLVIHSEQVHTQHPNLTEATVQPLDPDLTITPQPTTEGELPQTLQDSTSQIII

A;Experimental source: strain Bristol N2; clone F16F9 C;Genetics: A;Gene: CESP:F16F9.2 A;Map position: X A;Introns: 35/1; 361/1; 384/1; 482/2; 517/1; 971/1; 1021/2; 1179/3 Query Match Best Local Similarity 23.8%; Pred. No. 5e-11; Matches 365, Conservative 107; Mismatches 388; Indels 673; Gaps 75; QY 2 AMTILPIYLLILISVEVIQOVSSQLISSCAGRCGEGYSRDATCNCDYNCQHYMECCPDFK 61	38 IVKHIKKNTČT	APTTEREPAPTTERE PAPTTREADTTPKEPAPTAPKRAPTTPKEP GPATGKPETTHFPUTGTTPNFDTATETPFVAKSEDKMTLSKTAATETTQ:  GPATGKPETTHFPUTGTTPNFDTATETPFVAKSEDKMTLSKTAATETTQ:  APTTEREPAPTTTKEPSPTTFKEPAPTTTKSAPTTTKEFPAPTTT  TEVT-DGPEKETTKNVSIEIPITTVPLVETTSTTSKESDGFHTTLKLKVTTADSDST  KSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAP	552 PEELAPTTPEEPTTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKET 611 590KPTTTQESVSTEKTSTTKKASTTEEPTTTDEPTTTTESSTTGKAT 634 612 APTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGT 664 635 TPELSTTSETTTTELKITTEGSTTTEEPTTTAIFABASTGIITTDEET 683 665 APTTPKEPAPTTPKEPAPTTLKEPAPTTLKEPAPTTP
Qy         938		QY         1161	RESULT 14 T25697 hypothetical protein F16F9.2 - Caenorhabditis elegans C; Becies: Caenorhabditis elegans C; Becies: Caenorhabditis elegans C; Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C; Accession: T25697 R; Pullon, B S; Submitted to the EMBL Data Library, August 1996 A; Description: The sequence of C: elegans cosmid F16F9. A; Reference number: Z20071 A; Reference number: Z20071 A; Recession: T25697 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Releas: DNA A; Residues: DNA A; Residues: L-1229 eFUL.> A; Cross-references: UNIPROT: Q94185; EMBL: U67956; PIDN: AAB07691.1; GSPDB: GN00028; CESP: F1

δy	746 PKKPAPTTPETPPPTTSE-VSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKE 802
Db	802 TITIEKITSKITTEKPITSESATIETITSEPSTTEST838
Qy	803 PGVPTTKTPAATKPEMITTAKDKTTBRDLKTTTA
QQ	839TVDISSATTEESSTAAETTITSAETSETTISESAAFITGESPENTALQSSSQK 891
δλ	841APKOTKETAITIEKTIESKITATTTQ-VISTTIQDTIPFK 879
qq	892 SEENESSAEKPGARRDFVPKKHKTTVKPAETTSAVAASTTTTEPITTTEKSTTLETTPIE 951
ò	880 ITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQ 929
QQ	952 ATTLNEVTGPAFVTGAPVDETTINTLELLSKINNTQISQPKPTDISKTDA 1001
δ	930KPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELN 970
Ob	1002 LSSLISGLIGSFTKAPMAPTIHTTTDAAFVTATEASLNDGSDKKIID 1048
ò	971PTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTP 1027
qo	1049 EAQPIDEIRRAQPINQPTN
ò	1028 DMDYLPRVPNQGIII 1046
qq	1068 EMEFEKRIREQRIQMEQAKRLREBELLEKQLQBQEIEEKARNEMIERKQKMLQQLBELKE 1127
ò	1047SDETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSP 1082
Db	1128 ABERQRVLLEQERLQEQERQRLIAEKEAEIAFGSISTTTEASKFKYR 1174
δý	1083 FSPPSPARRITEVWGIPSPIDTVFTRCNCE-GKTFFFKDSQYWRFTNDIKDAGYP 1136
QQ	1175LRPAQCAAINKFTRVFNITDPSEWIQKNCEFAKRYFPBASCP 1216
δ	1137 KPIFKGFGGLTGQIVAALSTAKYKNWPESVYFF 1169
DÞ	1217QIQALIESCFAF 1228

Cypecies: Homo sapiens (man)
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Cypecies: Homo sap mucin 1 precursor, repetitive splice form A [validated] - human
N;Alternate names: breast carcinoma-associated DF3 antigen; core protein KP39; episialin
ncreatic mucin; polymorphic epithelial mucin (PEM)
N;Contains: mucin 1 precursor, epithelial tumor antigen splice form; mucin 1 precursor,

sednence A; Molecule type: mRNA
A; Residues: 1-19, 29-992,1033-1344 < GEN>
A; Cross-references: GB:105581; NID:9188869; PIDN:AAA59876.1; PID:9188870
A; Cross-references: GB:105581; NID:9188869; PIDN:AAA59876.1; PID:9188870
A; Note: GenBank entry HUMMUCAB includes one copy of the tandemly repeated in the note; Batra, S.K.; Qi, W.N.; Metzgar, R.S.; Hollingsworth, M.A.
J; Batol. Chem. 265, 15294-15299, 1990
A; Title: Cloring and sequencing of a human pancreatic tumor mucin cDNA.
A; Reference number: A35887; WUID:90368716; PMID:2394722
A; Accession: A35887

A; Molecule type: mRNA

A;Residues: 119,29-1109,'S',1111-1339,'A',1341-1344 <LAN>
A;Cross-references: GB:105582; NID:9189598; PIDN:AAA6019.1; PID:9189599
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A;Note: GenBank entry HUMRANMU contains four fewer copies of the tandemly repeated seque R;Wreschner, D.H.; Hareuveni, M.; Tsarfaty, I.; Smorodinsky, N.; Horev, J.; Zaretsky, J. Bur. J. Blochem. 189, 463-473, 1990
A;Title: Human epithelial tumor antiqen cDNA sequences. Differential splicing may general A;Reference number: S10571; MUID:90276413; PMID:2351132

A;Accession: S10572

A,Molecule type: mRNA A,Residues: 1-19,29-155,'P',157-175,'P',177-182,'A',184-212,1033-1344 <WRE> A,Cross-references: BMBL:X52229; NID:g37053 R,Wreschner, D.H. submitted to the EMBL Data Library, March 1990

A; Reference number: S40293 A; Accession: S40293

A; Molecule type: mRNA A; Residues: 1-19,29-155, P',157-175, P',177-182, A',184-212,1033-1037, A',1039-1344 < WR2 A; Cresidues: 1-19,29-155, P', 157-175, P',177-182, A',184-212,1033-1037, A', 1039-1344 < WR2 A; Creenenes: EMBL:X5229; NID:937053; PIDN:CAA36478.1; PID:937054 R; Abe, M.; Siddiqui, J.; Kufe, D. Biochem. Biophys. Res. Commun. 165, 644-649, 1989 A; Titles: Sequence analysis of the 5' region of the human DF3 breast carcinoma-associated A; Reference number: A36735; MUID:90088473; PMID:2597151

A, Molecule type: mRNA
A, Residues: 1-142, 'Q', 144-162, 'Q', 164-168 < ABE>
A, Residues: 1-143, 'Q', 144-162, 'Q', 164-168 < ABE>
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A, Residues: 1-143, 'Q', 144-162, 'Q', 164-168 < ABE>
A, Cross-references: EMBL: M3183; NID: 9181842; PIDN: AABA35757.1; PID: 9181543
A, Malecule and Lore protein as well as polymorphic epithelial mucin carry peanut agglu
A, Reference number: JX0235; MUID: 93123189; PMID: 1478919
A, Accession: PX006
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 998-1011, 'ES', 1014-1017; 1018-1032, 'T', 1034-1037; 1038-1057 < MAS>
A, Residues: 998-1011, 'ES', 1014-1017; 1018-1032, 'T', 1034-1037; 1038-1057 < MAS>
A, Residues: 136, 130-136, 1994
A, Rizinan-Licht, S: Baruch, A: Elroy-Stein, O: Keydar, I:; Wreschner, D.H.
PEBS Lett. 356, 130-136, 1994
A, Reference membrane proteins cytokine x
A, Reference number: S51026; MUID: 95080414; PMID: 7988707

A; Note: undetermined: Soluze; MolDisysOs0414; PMID: 98870,
A; Note: undetermined tyrosine residues in the carboxyl-terminal non-repetitive region as C; Comment: This protein is length polymorphic. Individuals may have between 21 and 125 c; Comment: This protein is length polymorphic. Individuals may have between 21 and 125 c; Comment: Serine and threonine residues in the tandem repeat domain are extensively gly C; Comment: For an alternative splice form without a tandem repeat domain, see PIR:548146 C; Comment: For an alternative splice form without a tandem repeat domain, see PIR:548146 A; Gross-references: GDB:120705; OMIM:158340
A; Gross-references: GDB:120705; OMIM:158340
A; Gross-references: GDB:120705; OMIM:158340
A; Map position: 1421-1423
A; Introns: 20/1; 62/3; 1165/3; 1184/2; 1230/1; 1270/3; 1320/3
C; Superfamily: polymorphic epithelial mucin
C; Keywords: alternative splicing; duplication; glycoprotein; phosphoprotein; polymorphis F; 1-1344/Product: mucin | amino-terminal non-repetitive
F; 1-23/Domain: signal sequence #link PREB #status predicted <SIGB>F; 1-19, 29-1344/Product: mucin | precursor, splice form B #status predicted <PREB>F; 1-19, 29-212, 1033-1344/Product: mucin | precursor, epithelial tumor antigen splice form F; 1-19, 29-212, 1033-1344/Product: mucin | precursor, epithelial tumor antigen splice form F; 1-10, 29-212, 1033-1344/Product: mucin | precursor, epithelial tumor antigen splice form F; 1-10, 29-212, 1033-1344/Product: mucin | precursor, epithelial tumor antigen splice form F; 1-10, 29-212, 1033-1344/Product: mucin | precursor, epithelial tumor antigen splice form F; 1-10, 29-212, 1033-1344/Product: mucin | precursor, epithelial tumor antigen splice form F; 1-10, 20-212, 1033-1344/Product: mucin | precursor, epithelial tumor antigen splice form F; 1-10, 20-212, 1033-1344/Product: mucin | precursor, epithelial tumor antigen splice form F; 1-10, 20-212, 103-1040, 20-212, 103-212, 103-212, 103-212, 103-212, 103-212, 103-212, 103-212, 103-212, 103-212, 103-212, 103-212, 103-212, 103-

Fil143-1344/Region: mucin 1 carboxyl-terminal non-repetitive Fil245-1272/Domain: transmembrane #status predicted <TRN> Fil046,1064,1118,1144,1222/Binding site: carbohydrate (Asn) (covalent) #status predictec F;1213/Binding site: phosphate (Tyr) (covalent) #status predicted

th 1344; ls 815; Gaps 84;	HYMECCPDFKRVCTA 66	18	KNRTKKKPTPKPPVV 126	18	PPNSDTSKETSLTVN 186	TATTAP 24		S 80	-STTPKE 272        GSTTPPAHDVTSAPDNK 134	APITIKEPA 312	AHGVT	-KKPAPTTPKEP 358	:    : TRPAPGSTAPPAHGV 247	-APTTPKEPAPTAP 394	TRPAPGSTAPPAHGV 307	-SPITPKEPAPTIK 435	:  PDTRPAPGSTAPP 363	APTTPKEPAP 477	RPAPGSTAPPAHGVTSAPDTRPAPGS 419	<b>A</b> PTTTKKPAP 509	HGVTSAPDTRPAPGS 479	ELAPTIPEEPTP 565	HGVTSÅPDTRPAPGS 539	KEPAPTT 599    : HGVTSAPDTRPAPGS 599	62	65	1	:         TAPPAHGVTSAPDTR 714	TTPKK 703	: :TAPPAHGVTSAPDTR 774	PTTPK 747
12.3%; Score 867.5; DB 1; Length larity 21.8%; Pred. No. 7.1e-11; Conservative 93; Mismatches 423; Indels	PIYLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDFKRVCTA	:    :  PFFLLLLLLTTUL	ELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVKDNKKNRTKKKPTPKPPVV		DBAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVN		EI	KETSATORSSVÞSSTEKNAV	TTKCPALTTPKEPTPTTPKEPAKB 	TIKSAPITPKEPAPITTKSAPTTPKEPAPITTKEP	:             PAHGVISAPDIRPAPGSIAPPAHGVISAPDI	PITPKEPAPITIKEPAPITIKSAPITPKEPAPITP	RPAPGSTAPPAHGVT-SAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGV RPAPGSTAPPAHGVT-SAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGV	-APTTEKEPTPTTPKEPAPTTKEPAP	TSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGV	KKPAPTTYEEPAPTTPKEPAPTTYEEP		SAPITIKEPAPITIKSAPITPKEPSPITIKEP	AHGVISAPDIRPAPGSIAPPAHGVISAPDIRPAPGSIAPP	KKPAPTTPKBPAPTTPKEP	TAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGS	TAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPE-	TAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGS	TTPEBPAPTTPKAAAPNTPKEPAPTTPKEPAPTT 	PAPTTPKETAPTTPKG-	PAHGVTSAPDTRPAPG	KKPAPKELAPTTTKEPTSTTSDKPAPTTPKG-		KEPAPITPKEPAPTTPKGTAPITLKEPAPITP		PAPKELAPTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTP
Query Match Best Local Similarity Matches 371; Conser	Oy 7 PIYI	:   	QY 67 ELSC	61 dd	Oy 127 DEA(	Db 19	187	25	Oy 245 TTK(	Oy 273 PTPTT		Oy 313 PTTI	191 PDT.	Oy 359AI	Db 248 TSAI	Qy 395	Db 308 TSA	Qy 436	Db 364 AHG	478	Db 420 TAPI	510	Db 480 TAPI	Oy 566 TTP-       Db 540 TAP	009	009	Qy 630 TTP.	Db 660 TAP	Qy 670 KEP	   0b 715 PAP	OV PAP

Search completed: October 13, 2004, 12:03:35 Job time : 106.704 secs

PPITSEVSTPITIKEPITIHKSPDESIPELSAEPIPKALENSP 800	-  TAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAP 891	PAATKPEMITIAKDKTIERDLRITPETTTAAP 842	DTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAP 951	KMIKETATITEKITIESKITATITQVISTTIQDTTPFKITTLLAPKVITIKKIITIT 902	1	EIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKM 962	APGSTAPPAHGVTSAPDTRPAGSTAPPAHGVTSAPDTRPAPGSTAPPAHG 1006	ISRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLL 1016	VISAPDTRPAPGSTAPPAHGVTSAPDNRPALGSTAPPVHNVTSASGSASG 1056	RPHVEMPEVTPDMDYLPRVPNQGIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHY 1076		FWMLSPFSPPARRITEVWGIPSPIDIVFTRCNCEGKT1115	SHHSDTPTTLASHSTKTDASSTHHSTVPPLTSSNHSTS 1122	FKDSQYWRFTNDIKDAGYPKPIFKGFGGLT- 1147	PQLSTGVSFFFLSFHISNLQFNSSLEDPSTDYYQELQRDISEMFLQIYKQGGFLGLSN 1180	-GQIVAALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQK 1187	VITLAFREGIINVHDVETQFNQYKTEAASRYNLTISDVS 1229	1192 1192	VSDVPFPFSAQSGAGVPGWGIALLVLVCVLVALAIVYLIALAVCQCRRKNYGQLDIFPAR 1289	PALNYPOYGEMTQVRRRRFERAIGPSQTHTIRIQXSPARLAYQDKG 1238	LYHTHGRYVPPSSTDRSPYEKVSAGNGGSSLSYTNPA 1336	WRGLPNVVTSA 1260	AATSA 1342
KPAPTTP	RPAPGS-	KEPGVPTTKTPAA	N		2		-	TSTMPELNP			7		TPFSIPS	6FFF		!	1 IKFRPGSVVVQLTLA	8		1	DTYHPMSEYPTY	9 VLHNEVKVSILWRGLPNVVTSA	VV
748	834	801	892	843	952	903	926	963	1007	1017	1057	1077	1079	1116	1123	1148	1181	1188	1230	1193	1290	1239	1337
δ	qq	à	Op	Š	qq	ò	qq	δ	QQ	δy	qq	δy	ΩP	Ωy	qq	ò	qq	δ	qq	δ	OP	δ	qq

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